

EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 14  
LENGTH: 1293  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-182-145-14

Query Match 5.0%; Score 32; DB 4; Length 1293;  
Best Local Similarity 100.0%; Pred. No. 16e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCCTGCTGCTGATGCTGCTGCTG 406  
DB 1146 GTACCCCTGCTGCTGATGCTGCTGCTG 1115

RESULT 6  
US-09-182-145-117

Sequence 117, Application US/09182145B  
Patent No. 6387657

GENERAL INFORMATION:

APPLICANT: Botstein, David A.

APPLICANT: Cohen, Robert

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Lawrence, David A.

APPLICANT: Levine, Arnold J.

APPLICANT: Pennica, Diane

APPLICANT: Roy, Margaret Ann

APPLICANT: Wood, William I.

TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: P1176R2

CURRENT APPLICATION NUMBER: US/09/182,145B

CURRENT FILING DATE: 1998-10-29

EARLIER APPLICATION NUMBER: US 60/063,704

EARLIER FILING DATE: 1997-10-29

EARLIER APPLICATION NUMBER: US 60/073,612

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: US 60/081,695

EARLIER FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 156

SEQ ID NO 117

LENGTH: 51

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1-51

OTHER INFORMATION: Sequence is synthesized.

Patent No. 6387657

US-09-182-145-117

Query Match 4.3%; Score 27; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.00043;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 380 CCTGCTGCTGATGCTGCTGCTGCTG 406  
DB 1 CCTGCTGCTGATGCTGCTGCTGCTG 27

RESULT 7  
US-09-385-982-220/c

Sequence 220, Application US/09385982

Patent No. 6262334

GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

FILE REFERENCE: CC DNA-260XX

CURRENT APPLICATION NUMBER: US/09/385,982

CURRENT FILING DATE: 1999-08-30  
EARLIER APPLICATION NUMBER: 09/328,111  
EARLIER FILING DATE: 1999-06-08  
EARLIER APPLICATION NUMBER: 60/117,393  
EARLIER FILING DATE: 1999-01-27  
EARLIER APPLICATION NUMBER: 60/098,639  
EARLIER FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 544  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 220

LENGTH: 616

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(616)

OTHER INFORMATION: n = A,T,C or G

US-09-385-982-220

Query Match 3.0%; Score 19; DB 4; Length 616;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 617 TGATGACGCTGCTTCACC 635  
DB 127 TGATGACGCTGCTTCACC 109

RESULT 8  
US-09-182-145-39

Sequence 39, Application US/09182145B

Patent No. 6387657

GENERAL INFORMATION:

APPLICANT: Botstein, David A.

APPLICANT: Cohen, Robert

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Lawrence, David A.

APPLICANT: Levine, Arnold J.

APPLICANT: Pennica, Diane

APPLICANT: Roy, Margaret Ann

APPLICANT: Wood, William I.

TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: P1176R2

CURRENT APPLICATION NUMBER: US/09/182,145B

CURRENT FILING DATE: 1998-10-29

EARLIER APPLICATION NUMBER: US 60/063,704

EARLIER FILING DATE: 1997-10-29

EARLIER APPLICATION NUMBER: US 60/073,612

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: US 60/081,695

EARLIER FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 156

SEQ ID NO 39

LENGTH: 841

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1-841

OTHER INFORMATION: Sequence is synthesized.

Patent No. 6387657

US-09-182-145-39

Query Match 3.0%; Score 19; DB 4; Length 841;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 388 TGGATGCTGCTGCTGCTG 406  
DB 151 TGGATGCTGCTGCTGCTG 169

RESULT 9  
US-09-149-476-225/C  
Sequence 225, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11

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EARLIER FILING DATE: 1997-04-11  
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EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056,845  
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EARLIER FILING DATE: 1997-08-22  
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      3.0%; Score 19; DB 4; Length 1196;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      617 TGATGCGTGGCTCACC 635
DB      134 TGATGCGTGGCTCACC 116

RESULT 10
US-09-149-476-57/c
; Sequence 57, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002pl
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/057, 650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056, 884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057, 669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049, 610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061, 060  
EARLIER FILING DATE: 1997-10-02

Query Match 3.0%; Score 19; DB 4; Length 1220;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TGATGACGGCTGCAC 635  
Db 128 TGATGACGGCTGCAC 110

RESULT 11  
US-09-213-768-1/c  
Sequence 1, Application US/09213768  
Patent No. 5985664  
GENERAL INFORMATION:  
APPLICANT: Brenda F. Baker  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRYIN EXPRESSION  
FILE REFERENCE: RTS-0026  
CURRENT APPLICATION NUMBER: US/09/213,768  
CURRENT FILING DATE: 1998-12-17  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 1

LENGTH: 1514  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (136)..(441)  
US-09-213-768-1

Query Match 3.0%; Score 19; DB 2; Length 1514;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 617 TGATGACGGTGCTTCACC 635  
|||||  
DB 136 TGATGACGGTGCTTCACC 118

## RESULT 12

US-09-668-680-13  
Sequence 13, Application US/09668680  
Patent No. 6436703

## GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Zhou, Ping  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Wang, Jian-kui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6436703el Nucleic Acids and  
FILE REFERENCE: 790CIP2A  
CURRENT APPLICATION NUMBER: US/09/668,680  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: pl\_FL-genes Version 2.0  
SEQ ID NO 13  
LENGTH: 1539  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (130)..(1539)  
US-09-668-680-13

Query Match 3.0%; Score 19; DB 4; Length 1539;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 CTCTCTGCGCTCTCTCA 305  
|||||  
DB 774 CTCTCTGCGCTCTCTCA 792

## RESULT 13

US-09-213-768-2/c  
Sequence 2, Application US/09213768  
Patent No. 5985664

## GENERAL INFORMATION:

APPLICANT: Brenda F. Baker  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION  
FILE REFERENCE: RTS-0026  
CURRENT APPLICATION NUMBER: US/09/213,768  
CURRENT FILING DATE: 1998-12-17  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 2

LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR Primer  
US-09-213-768-2

Query Match 2.8%; Score 18; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 617 TGATGACGGTGCTTCAC 634  
|||||  
DB 18 TGATGACGGTGCTTCAC 1

## RESULT 14

US-08-259-451-10  
Sequence 10, Application US/08259451  
Patent No. 6406841

## GENERAL INFORMATION:

APPLICANT: Lee, Helen H.  
APPLICANT: Swanson, Priscilla A.  
APPLICANT: Idler, Kenneth B.  
APPLICANT: Rosenblatt, Joseph D.  
APPLICANT: Chen, Irvin S. Y.  
APPLICANT: Golde, David W.  
APPLICANT: Robertson, Eugene F.  
APPLICANT: Stephens, John E.  
APPLICANT: Chan, Emerson W.  
APPLICANT: Bytendorp, Mark H.  
APPLICANT: Johnson, Joan E.  
APPLICANT: Motley, Cheryl T.  
APPLICANT: Peterson, Bryan  
APPLICANT: Edwards, Michelle  
APPLICANT: Guidinger, Peggy  
APPLICANT: Tate, Cynthia  
TITLE OF INVENTION: HTLV-IIIRN Compositions  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: One Abbott Park Road  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
MEDIUM TYPE: storage  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,451  
FILING DATE: 20-JUN-1994  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/086,415  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Daniel W. Collins  
REGISTRATION NUMBER: 31,912  
REFERENCE/DOCKET NUMBER: 5381.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 937-6365  
TELEFAX: (708) 938-2623  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2949 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear

US-08-259-451-10

Query Match 2.8%; Score 18; DB 4; Length 2949;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 193 GGCCTCAGCGCCTCACC 210  
IIIIIIIIIIIIIIIIIIII  
DB 2071 GGCCTCAGCGCCTCACC 2088

## RESULT 15

US-08-249-380-1/c  
; Sequence 1, Application US/08249380  
; Patent No. 5827685  
; GENERAL INFORMATION:  
; APPLICANT: Lindquist, Susan  
; TITLE OF INVENTION: Methods and Compositions of Genetic  
; TITLE OF INVENTION: Stress Response Systems  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/249,380  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/710,187  
; FILING DATE: 31-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: AKCD:024  
; TELEPHONE: 713-787-1400  
; TELEFAX: 713-789-2679  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3727 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-249-380-1

Query Match 2.8%; Score 18; DB 1; Length 3727;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 ACTGATCCACTCTCTGGC 280  
IIIIIIIIIIIIIIIIIIII  
DB 1143 ACTGATCCACTCTCTGGC 1126

Search completed: July 28, 2003, 15:58:54  
Job time : 35.7003 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:30:21 ; Search time 156.381 Seconds  
(without alignments)  
8377.033 Million cell updates/sec

Title: US-10-010-408-1\_COPY\_1\_635  
Perfect score: 635  
Sequence: 1 GACGCTCTGATCTCCAGAG.....GTGATGACGGTGCCTCACC 635

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1439767 seqs, 1031500376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCIT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	635	100.0	US-10-010-408-1	Sequence 1, App1
2	387	60.9	US-10-010-408-3	Sequence 3, App1
3	318	50.1	US-10-010-408-12	Sequence 12, App1
4	210	33.1	US-10-010-408-8	Sequence 8, App1
5	90	14.2	US-10-010-408-5	Sequence 5, App1
6	90	14.2	US-10-112-267-17	Sequence 17, App1
7	90	14.2	US-10-112-267-18	Sequence 18, App1
8	32	5.0	US-10-112-267-38	Sequence 38, App1
9	32	5.0	US-10-137-866-319	Sequence 319, App
10	32	5.0	US-10-146-726-319	Sequence 319, App
11	32	5.0	US-10-146-727-319	Sequence 319, App
12	32	5.0	US-10-146-788-319	Sequence 319, App
13	32	5.0	US-10-152-380-319	Sequence 319, App
14	32	5.0	US-10-153-934-319	Sequence 319, App
15	32	5.0	US-10-028-072-319	Sequence 319, App
16	32	5.0	US-10-121-049-319	Sequence 319, App

17	32	5.0	US-10-123-904-319	Sequence 319, App
18	32	5.0	US-10-140-470-319	Sequence 319, App
19	32	5.0	US-10-175-746-319	Sequence 319, App
20	32	5.0	US-10-176-918-319	Sequence 319, App
21	32	5.0	US-10-176-921-319	Sequence 319, App
22	32	5.0	US-10-137-865-319	Sequence 319, App
23	32	5.0	US-10-140-474-319	Sequence 319, App
24	32	5.0	US-10-142-431-319	Sequence 319, App
25	32	5.0	US-10-143-114-319	Sequence 319, App
26	32	5.0	US-10-140-002-319	Sequence 319, App
27	32	5.0	US-10-142-419-319	Sequence 319, App
28	32	5.0	US-10-123-262-319	Sequence 319, App
29	32	5.0	US-10-142-423-319	Sequence 319, App
30	32	5.0	US-10-121-050-319	Sequence 319, App
31	32	5.0	US-10-141-755-319	Sequence 319, App
32	32	5.0	US-10-143-032-319	Sequence 319, App
33	32	5.0	US-10-123-108-319	Sequence 319, App
34	32	5.0	US-10-123-236-319	Sequence 319, App
35	32	5.0	US-10-123-261-319	Sequence 319, App
36	32	5.0	US-10-140-921-319	Sequence 319, App
37	32	5.0	US-10-140-828-319	Sequence 319, App
38	32	5.0	US-10-121-045-319	Sequence 319, App
39	32	5.0	US-10-123-292-319	Sequence 319, App
40	32	5.0	US-10-123-903-319	Sequence 319, App
41	32	5.0	US-10-124-819-319	Sequence 319, App
42	32	5.0	US-10-124-822-319	Sequence 319, App
43	32	5.0	US-10-140-925-319	Sequence 319, App
44	32	5.0	US-10-160-498-319	Sequence 319, App
45	32	5.0	US-10-124-824-319	Sequence 319, App

ALIGNMENTS

RESULT 1  
US-10-010-408-1  
Sequence 1, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castelli et al., Jr.  
TITLE OF INVENTION: No. US20020165185A1et1 Heparin-Induced CCN-Like Molecules and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandiagouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1708 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 249..1001  
SEQUENCE DESCRIPTION: SEQ ID NO: 1  
US-10-010-408-1

Query Match 100.0%; Score 635; DB 15; Length 1708;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGCTTCGATCTCCAGAGAGACCCCTGGGGTGGAGACAGGCGCTTGGACAGCTGAGCC 60  
1 GACGCTTCGATCTCCAGAGAGACCCCTGGGGTGGAGACAGGCGCTTGGACAGCTGAGCC 60  
DB 1 GACGCTTCGATCTCCAGAGAGACCCCTGGGGTGGAGACAGGCGCTTGGACAGCTGAGCC 60  
QY 61 GCTGGGCACTGCTTGGATGAGAGCTTATTACTGGGAACTGAGAGAGCTAAGAGGCTC 120  
61 GCTGGGCACTGCTTGGATGAGAGCTTATTACTGGGAACTGAGAGAGCTAAGAGGCTC 120  
DB 121 CTCTCAGCTTGTCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 180  
121 CTCTCAGCTTGTCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 180  
QY 181 CACCTTCGTGTGCTCCAGAGGCTCCACCTTCAGGTTGAACTGAGCTGAGCTGAGAGGAC 240  
181 CACCTTCGTGTGCTCCAGAGGCTCCACCTTCAGGTTGAACTGAGCTGAGCTGAGAGGAC 240  
DB 181 CACCTTCGTGTGCTCCAGAGGCTCCACCTTCAGGTTGAACTGAGCTGAGCTGAGAGGAC 240  
QY 241 ACGGTGACATGAGAGGAGGAGCCACATGATCCATCTTGGGCACTTCTCTCTGCTTC 300  
241 ACGGTGACATGAGAGGAGGAGCCACATGATCCATCTTGGGCACTTCTCTCTGCTTC 300  
DB 241 ACGGTGACATGAGAGGAGGAGCCACATGATCCATCTTGGGCACTTCTCTCTGCTTC 300  
QY 301 TCTCATGCTGTGTGCTCCAGCTGTGCGGAGACACCTCTGCTCTCTTGGACACACCC 360  
301 TCTCATGCTGTGTGCTCCAGCTGTGCGGAGACACCTCTGCTCTCTTGGACACACCC 360  
DB 301 TCTCATGCTGTGTGCTCCAGCTGTGCGGAGACACCTCTGCTCTCTTGGACACACCC 360  
QY 361 AGTGGCCACAGGGGGTACCCCTGGTGTGATGGTGGCTGCTCTGCTGCTGCTGCTGCTG 420  
361 AGTGGCCACAGGGGGTACCCCTGGTGTGATGGTGGCTGCTCTGCTGCTGCTGCTGCTG 420  
DB 361 AGTGGCCACAGGGGGTACCCCTGGTGTGATGGTGGCTGCTCTGCTGCTGCTGCTGCTG 420  
QY 421 GGAGGCTGGGGAGTCTCTGCGACACCTGATGTGCGACCCACCCAGGAGGCTGCTT 480  
421 GGAGGCTGGGGAGTCTCTGCGACACCTGATGTGCGACCCACCCAGGAGGCTGCTT 480  
DB 421 GGAGGCTGGGGAGTCTCTGCGACACCTGATGTGCGACCCACCCAGGAGGCTGCTT 480  
QY 481 GTGAGCTGGGGAGGAGGCTTGGGCGCATGGGGCTGTGTCTCTTGGATGAGAGATGACG 540  
481 GTGAGCTGGGGAGGAGGCTTGGGCGCATGGGGCTGTGTCTCTTGGATGAGAGATGACG 540  
DB 481 GTGAGCTGGGGAGGAGGCTTGGGCGCATGGGGCTGTGTCTCTTGGATGAGAGATGACG 540  
QY 541 GTAGCTGTGAGTGAATGGCGCAGAGTACCTGGATGAGAGACCTTAAACCAATTGCA 600  
541 GTAGCTGTGAGTGAATGGCGCAGAGTACCTGGATGAGAGACCTTAAACCAATTGCA 600  
DB 541 GTAGCTGTGAGTGAATGGCGCAGAGTACCTGGATGAGAGACCTTAAACCAATTGCA 600  
QY 601 GGGTCTGTGCTGCTGTGATGAGCGGTGCTTCAAC 635  
601 GGGTCTGTGCTGCTGTGATGAGCGGTGCTTCAAC 635  
DB 601 GGGTCTGTGCTGCTGTGATGAGCGGTGCTTCAAC 635

RESULT 2  
US-10-010-408-3

Sequence 3, Application US/10010408  
Publication No. US20020165185A1

GENERAL INFORMATION:

APPLICANT: John J. Castelli, Jr.

TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408

FILING DATE: 07-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/044,273

FILING DATE: March 19, 1998

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragoras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MBI-004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 753 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

FEATURE:

NAME/KEY: CDS

LOCATION: 1..750

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-010-408-3

Query Match 60.9%; Score 387; DB 15; Length 753;

Best Local Similarity 100.0%; Pred. No. 2,6e-194;

Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 ATGAGGGGAGAGCCCATGATCCATCTTGTGGCCACTTCTCTCTGCTTCTGCTTCTGCTT 308  
1 ATGAGGGGAGAGCCCATGATCCATCTTGTGGCCACTTCTCTCTGCTTCTGCTTCTGCTT 308  
DB 1 ATGAGGGGAGAGCCCATGATCCATCTTGTGGCCACTTCTCTCTGCTTCTGCTTCTGCTT 308  
QY 309 GTGTGTGCCAGCTGTGCGGAGACACCTGTACTGTCTTGGACACACCCAGTGCCTCA 368  
309 GTGTGTGCCAGCTGTGCGGAGACACCTGTACTGTCTTGGACACACCCAGTGCCTCA 368  
DB 309 GTGTGTGCCAGCTGTGCGGAGACACCTGTACTGTCTTGGACACACCCAGTGCCTCA 368  
QY 61 GTGTGTGCCAGCTGTGCGGAGACACCTGTACTGTCTTGGACACACCCAGTGCCTCA 120  
61 GTGTGTGCCAGCTGTGCGGAGACACCTGTACTGTCTTGGACACACCCAGTGCCTCA 120  
DB 61 GTGTGTGCCAGCTGTGCGGAGACACCTGTACTGTCTTGGACACACCCAGTGCCTCA 120  
QY 369 CAGGGGATACCCCTGTGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 428  
369 CAGGGGATACCCCTGTGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 428  
DB 369 CAGGGGATACCCCTGTGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 428  
QY 121 CAGGGGATACCCCTGTGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
121 CAGGGGATACCCCTGTGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
DB 121 CAGGGGATACCCCTGTGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
QY 429 GGGGATCTCTGCGACACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488  
429 GGGGATCTCTGCGACACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488  
DB 429 GGGGATCTCTGCGACACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488  
QY 181 GGGGATCTCTGCGACACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
181 GGGGATCTCTGCGACACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GGGGATCTCTGCGACACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 489 GGGGAGGCGCTTGGCGCATGGGGCTGTGTCTCTTGGATGAGAGTACGCTGCT 548  
489 GGGGAGGCGCTTGGCGCATGGGGCTGTGTCTCTTGGATGAGAGTACGCTGCT 548  
DB 489 GGGGAGGCGCTTGGCGCATGGGGCTGTGTCTCTTGGATGAGAGTACGCTGCT 548  
QY 241 GGGGAGGCGCTTGGCGCATGGGGCTGTGTCTCTTGGATGAGAGTACGCTGCT 300  
241 GGGGAGGCGCTTGGCGCATGGGGCTGTGTCTCTTGGATGAGAGTACGCTGCT 300  
DB 241 GGGGAGGCGCTTGGCGCATGGGGCTGTGTCTCTTGGATGAGAGTACGCTGCT 300  
QY 549 GAGGTGAATGGCGCAGTACCTGATGAGAGACCTTAAACCAATTGACAGGCTCTG 608  
549 GAGGTGAATGGCGCAGTACCTGATGAGAGACCTTAAACCAATTGACAGGCTCTG 608  
DB 549 GAGGTGAATGGCGCAGTACCTGATGAGAGACCTTAAACCAATTGACAGGCTCTG 608  
QY 301 GAGGTGAATGGCGCAGTACCTGATGAGAGACCTTAAACCAATTGACAGGCTCTG 360  
301 GAGGTGAATGGCGCAGTACCTGATGAGAGACCTTAAACCAATTGACAGGCTCTG 360  
DB 301 GAGGTGAATGGCGCAGTACCTGATGAGAGACCTTAAACCAATTGACAGGCTCTG 360  
QY 609 TGGCGCTGTGATGAGCGGTGCTTCAAC 635  
609 TGGCGCTGTGATGAGCGGTGCTTCAAC 635  
DB 609 TGGCGCTGTGATGAGCGGTGCTTCAAC 635  
609 TGGCGCTGTGATGAGCGGTGCTTCAAC 635

RESULT 3

US-10-010-408-12

Sequence 12, Application US/10010408



Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castelljot, Jr.  
TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules  
and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 12:  
LENGTH: 681 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..681  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-010-408-12  
Query Match  
Best Local Similarity 50.1%; Score 318; DB 15; Length 681;  
Pred. No. 7.4e-158;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 318 CAGCTGTGCGGACACCCCTGTACCTGCTGTCGACACACCCCACTGCGGAGGTA 377  
DB 1 CAGCTGTGCGGACACCCCTGTACCTGCTGTCGACACACCCCACTGCGGAGGTA 60  
QY 378 CCCCTGTGTCGATGAGTGTGTCGCTGTAAGTGTGTCGACGAGGAGGCTGGGGAGTCC 437  
DB 61 CCCCTGTGTCGATGAGTGTGTCGCTGTAAGTGTGTCGACGAGGAGGCTGGGGAGTCC 120  
QY 438 TCGACACACCTGCATGTGTGCGACCCCAAGGCTGTTTGTCACTCGGGGCAAGC 497  
DB 121 TCGACACACCTGCATGTGTGCGACCCCAAGGCTGTTTGTCACTCGGGGCAAGC 180  
QY 498 CCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGATGACGAGTGTGAGTGTGAT 557  
DB 181 CCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGATGACGAGTGTGAGTGTGAT 240  
QY 558 GGGCCAGGTAAGTGTGATGAGAGACCTTTAAACCAATTGACAGGCTCTGTGCGCTGT 617  
DB 241 GGGCCAGGTAAGTGTGATGAGAGACCTTTAAACCAATTGACAGGCTCTGTGCGCTGT 300  
QY 618 GATGACGGTGGCTTCACC 635  
|||||

DB 301 GATGACGGTGGCTTCACC 318  
RESULT 4  
US-10-010-408-8  
Sequence 8, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castelljot, Jr.  
TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules  
and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 8:  
LENGTH: 210 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..210  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-010-408-8  
Query Match  
Best Local Similarity 33.1%; Score 210; DB 15; Length 210;  
Pred. No. 9.4e-101;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 318 CAGCTGTGCGGACACCCCTGTACCTGCTGTCGACACACCCCACTGCGGAGGTA 377  
DB 1 CAGCTGTGCGGACACCCCTGTACCTGCTGTCGACACACCCCACTGCGGAGGTA 60  
QY 378 CCCCTGTGTCGATGAGTGTGTCGCTGTAAGTGTGTCGACGAGGAGGCTGGGGAGTCC 437  
DB 61 CCCCTGTGTCGATGAGTGTGTCGCTGTAAGTGTGTCGACGAGGAGGCTGGGGAGTCC 120  
QY 438 TCGACACACCTGCATGTGTGCGACCCCAAGGCTGTTTGTCACTCGGGGCAAGC 497  
DB 121 TCGACACACCTGCATGTGTGCGACCCCAAGGCTGTTTGTCACTCGGGGCAAGC 180  
QY 498 CCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGATGACGAGTGTGAGTGTGAT 527  
DB 181 CCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGATGACGAGTGTGAGTGTGAT 210  
|||||

RESULT 5  
US-10-010-408-5  
Sequence 5, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castellot, Jr.  
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules  
and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..177  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-010-408-5  
Query Match 14.2%; Score 90; DB 15; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2.4e-37;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 546 TGTGAGGTGAGTGGCCGACAGTACCTGATGAGAGACGTTTAAACCAATTGCAGGGTC 605  
DB 1 TGTGAGGTGAGTGGCCGACAGTACCTGATGAGAGACGTTTAAACCAATTGCAGGGTC 60  
QY 606 CTGTGCGCTGTGATGAGCGTGGCTTCACC 635  
DB 61 CTGTGCGCTGTGATGAGCGTGGCTTCACC 90  
RESULT 6  
US-10-112-267-17  
Sequence 17, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/10/112,267  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 17  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-112-267-17  
Query Match 14.2%; Score 90; DB 15; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 2e-37;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 410 AGTGTGTGACGAGGAGCTGGGGAGTCCTGCGACACCTGATGTGTGGAGCCCGACCA 469  
DB 418 AGTGTGTGACGAGGAGCTGGGGAGTCCTGCGACACCTGATGTGTGGAGCCCGACCA 477  
QY 470 GGGCTGTGTTTGTGACCTGTGGGCGACGCC 499  
DB 478 GGGCTGTGTTTGTGACCTGTGGGCGACGCC 507  
RESULT 7  
US-10-112-267-18/c  
Sequence 18, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/10/112,267  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 18  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-112-267-18  
Query Match 14.2%; Score 90; DB 15; Length 1734;

Best Local Similarity 100.0%; Pred. No. 2e-37;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGACAGGAGGCTGGGGAGTCTCTGGACCACTGATGTCTCGACCCAGCCA 469  
Db 1117 AGTGTGACAGGAGGCTGGGGAGTCTCTGGACCACTGATGTCTCGACCCAGCCA 1258

OY 470 GGGCGTGTGTGTCAGCCTGGGCGAGGCC 499  
Db 1257 GGGCGTGTGTGTCAGCCTGGGCGAGGCC 1228

## RESULT 8

US-10-112-267-38  
Sequence 38, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/10/112,267  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 38  
LENGTH: 738  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-112-267-38

Query Match 5.0%; Score 32; DB 15; Length 738;

Best Local Similarity 100.0%; Pred. No. 9.e-07;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCGTGCTGAGTGGCTGCGCTGCG 406  
Db 115 GTACCCGTGCTGAGTGGCTGCGCTGCG 146

## RESULT 9

US-10-137-866-319  
Sequence 319, Application US/10137866  
Publication No. US20030129689A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C151  
CURRENT APPLICATION NUMBER: US/10/137,866  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059836  
PRIOR FILING DATE: 1997-09-24  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062285  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062814  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063550  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063561  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063704  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063733  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063735  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063738  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064248  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064809  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066453  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069212  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069278  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069334  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069694  
PRIOR FILING DATE: 1997-12-16  
PRIOR APPLICATION NUMBER: 60/072320  
PRIOR FILING DATE: 1998-01-23  
PRIOR APPLICATION NUMBER: 60/073612  
PRIOR FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: 60/074086  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/074092  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081695  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081818  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082999  
PRIOR FILING DATE: 1998-04-24  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085149  
PRIOR FILING DATE: 1998-05-12  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086414

PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/086430  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088730  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088741  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089539  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090538  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091982

Query Match 5.0%: Score 32; DB 14; Length 1266;  
Best Local Similarity 100.0%: Pred No. 9,2e-07;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GTACCCGTGCTGATGCTGTGCTGCTG 406  
Db 136 GTACCCGTGCTGATGCTGTGCTGCTG 167

RESULT 10  
US-10-146-726-319  
Sequence 319, Application US/10146726  
Publication No. US20030129690A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330RIC308

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; CURRENT APPLICATION NUMBER: US/10/146,726
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-726-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCCTGCTGCTGATGCTGCTGCTG 406
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DB 136 GTACCCCTGCTGCTGATGCTGCTGCTG 167

RESULT 11
US-10-146-727-319
; Sequence 319, Application US/10146727
; Publication No. US20030129691A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C312
; CURRENT APPLICATION NUMBER: US/10/146,727
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-727-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCCTGCTGCTGATGCTGCTGCTG 406
    |||||||
DB 136 GTACCCCTGCTGCTGATGCTGCTGCTG 167

RESULT 12
US-10-146-788-319
; Sequence 319, Application US/10146788
; Publication No. US20030129693A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C322
; CURRENT APPLICATION NUMBER: US/10/146,788
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-788-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCCTGCTGCTGATGCTGCTGCTG 406
    |||||||
DB 136 GTACCCCTGCTGCTGATGCTGCTGCTG 167

RESULT 13
US-10-152-380-319
; Sequence 319, Application US/10152380
; Publication No. US20030129694A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C397
; CURRENT APPLICATION NUMBER: US/10/152,380
; CURRENT FILING DATE: 2002-05-21
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-152-380-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      375 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 406
Db      136 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 167

RESULT 14
US-10-153-934-319
; Sequence 319, Application US/10153934
; Publication No. US20030129695A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C412
; CURRENT APPLICATION NUMBER: US/10/153,934
; CURRENT FILING DATE: 2002-05-22
; Prior Application removed - See file Wrapper or Balm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-153-934-319

Query Match      5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9, 2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 406
Db      136 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 167

RESULT 15
US-10-028-072-319
; Sequence 319, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; Prior Application removed - See file Wrapper or Balm
; NUMBER OF SEQ ID NOS:
; SEQ ID NO:
; LENGTH:
; TYPE:
; ORGANISM:

CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
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PRIOR FILING DATE: 1997-10-31
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PRIOR FILING DATE: 1997-10-24
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;; PRIOR FILING DATE: 1998-07-07

Query Match 5.0%; Score 32; DB 15; Length 1266;  
Best Local Similarity 100.0%; Pred. No. 9.2e-07;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 375 GRACCCGTGCTGTGATGCTGTGCTGCTG 406  
|||||  
Db 136 GRACCCGTGCTGTGATGCTGTGCTGCTG 167

Search completed: July 28, 2003, 15:36:32  
Job time : 157.381 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:16:26 ; Search time 1126.46 Seconds  
(without alignments)  
9129.604 Million cell updates/sec

Title: US-10-010-408-1\_COPY\_1\_635

Perfect score: 635  
Sequence: 1 GACGCTCTGATCTCCAGAG.....GTGATGACGTGCTTCACC 635

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estinu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	14.2	940	14	B0937887 AGNCOURT
2	67	10.6	537	14	B0560868
3	49	7.7	424	10	BB848097
4	32	5.0	380	12	BG900020
5	32	5.0	405	12	BG900069
6	32	5.0	618	12	BG538695

7	32	5.0	620	13	BG928868
8	32	5.0	651	13	B1457141
9	32	5.0	749	9	AL555144
10	32	5.0	750	13	BM043988
11	32	5.0	800	13	B1826781
12	32	5.0	886	13	B1822142
13	32	5.0	888	13	B1825652
14	32	5.0	916	13	B1457367
15	32	5.0	928	13	B161474
16	32	5.0	933	14	B0278961
17	32	5.0	979	14	B0279131
18	32	5.0	1006	14	BM921531
19	32	5.0	1058	14	BM805088
20	32	5.0	1073	14	B0073722
21	32	5.0	1166	13	BM543799
22	32	5.0	1251	14	B0961357
23	30	4.7	190	9	AA647775
24	23	3.6	436	17	AO095651
25	23	3.6	742	13	B1758148
26	23	3.6	792	13	B1823598
27	21	3.3	495	13	B1204749
28	21	3.3	529	9	A1897896
29	21	3.3	561	12	BF051668
30	21	3.3	563	9	A1897344
31	21	3.3	609	9	A1485142
32	21	3.3	620	10	AM223381
33	20	3.1	232	9	AL658941
34	20	3.1	251	9	A1303895
35	20	3.1	288	10	BE574058
36	20	3.1	332	17	A2650040
37	20	3.1	381	10	BE537338
38	20	3.1	391	20	A1147346
39	20	3.1	452	10	BE481184
40	20	3.1	475	9	AA862947
41	20	3.1	485	9	AA862518
42	20	3.1	488	9	AA630630
43	20	3.1	489	9	AA878562
44	20	3.1	509	9	AT002710
45	20	3.1	512	9	AA443583

#### ALIGNMENTS

RESULT 1  
B0937887

LOCUS

DEFINITION

AGENCOURT\_8951807 NCI\_CGAP\_Co24 Mus musculus cDNA clone

IMAGE:6476852 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

940 bp mRNA linear EST 21-AUG-2002

AGENCOURT\_8951807 NCI\_CGAP\_Co24 Mus musculus cDNA clone

IMAGE:6476852 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: L14M14017 row: n column: 21  
High quality sequence stop: 543.

location/Qualifiers  
1. 940

Query Match 14.2% Score 90; DB 14; Length 940;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-32;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 410 AGGTGTGCACGAGAGCTGGGAGAGTCCTGCGACACCTGCATGTCGACCCAGCCA 469  
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 444 AGGTGTGCACGAGAGCTGGGAGAGTCCTGCGACACCTGCATGTCGACCCAGCCA 503

Qy 470 GGCCCTGCTTGTTCAGCCTGGGAGAGCC 499  
 |||||||

Db 504 GGCCCTGCTTGTTCAGCCTGGGAGAGCC 533

BASE COUNT 169 a 277 c 288 g 200 t 6 others

ORIGIN

/organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_1ib="NCI CGAP\_C024"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt:  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI CGAP Library."

RESULT 2  
 B0560868 537 bp mRNA linear EST 20-JUN-2002  
 LOCUS H4067A01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone  
 DEFINITION H4067A01 5', mRNA sequence.  
 ACCESSION B0560868  
 VERSION B0560868.1 GI:21461753  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 537)  
 Vanburen,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin  
 P.R., Stagg,C.A., Bassey,U., Alba,K., Hamatani,T., Kargul,G.J.,  
 Luo,A.G. and Ko,M.S.H.  
 Assembly, verification, and initial annotation of NIA 7.4K mouse  
 cDNA clone set  
 Unpublished (2002)  
 CONTACT: Yong Qian  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA  
 Email: cdmelgusun.grc.nia.nih.gov  
 This clone set has been freely distributed to the community. Please  
 visit [http://lgsun.grc.nia.nih.gov/cDNA/NIA\\_7\\_4K.html](http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4K.html) for details.  
 Plate: H4067 row: A column: 01  
 Seq primer: -21M13 Reverse  
 High quality sequence stop: 537  
 POLYA-No.

FEATURES  
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 1. 537  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 /clone="H4067A01"  
 /clone\_1ib="NIA Mouse 7.4K cDNA Clone Set"  
 /sex="mixed"  
 /dev\_stage="mixed"  
 /lab\_host="DH10B"  
 /note="Vector: pSPORT1; site\_1: SalI; site\_2: NotI; This  
 clone is among a rearranged set of 7,407 clones from more  
 than 20 cDNA libraries."  
 87 a 162 c 166 g 122 t

BASE COUNT  
 ORIGIN

Query Match 10.6% Score 67; DB 14; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 3e-21;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 410 AGGTGTGCACGAGAGCTGGGAGAGTCCTGCGACACCTGCATGTCGACCCAGCCA 469  
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 Db 471 AGGTGTGCACGAGAGCTGGGAGAGTCCTGCGACACCTGCATGTCGACCCAGCCA 530

Qy 470 GGCCCTG 476  
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Db 531 GGCCCTG 537

RESULT 3  
 B8849097 424 bp mRNA linear EST 26-NOV-2001  
 LOCUS BB849097  
 DEFINITION BB849097 RIKEN full-length enriched, adult inner ear Mus musculus  
 cDNA clone F930006G02 5', mRNA sequence..  
 ACCESSION BB849097  
 VERSION BB849097.1 GI:17090551  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 424)

REFERENCE  
 AUTHORS Akimura,T., Arikawa,T., Carninci,P., Furuno,M., Hanagaki,T.,  
 Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii  
 Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,  
 Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,  
 Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,  
 Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa  
 A., Takahashi,F., Takaku-Akahara,S., Tanaka,T., Tomaru,A., Toya,T.,  
 Watabiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.  
 2001)

TITLE  
 JOURNAL  
 COMMENT Unpublished (2001)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.go.jp,  
 URL: <http://genome.gsc.riken.go.jp/>  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
 Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura  
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and  
 Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
 Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 noncyclopedic cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
 further details.  
 e mouse tissues.

FEATURES  
 source  
 1. 424  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="F930006G02"  
 /clone\_1ib="RIKEN full-length enriched, adult inner ear"

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/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cerebellum, dev_stage=0 day neonate,
sex-mixed", (tissue_type="hippocampus, dev_stage=adult,
sex-male), (tissue_type="whole body, dev_stage=9 days
embryo, sex-mixed), (tissue_type="lung, dev_stage=13 days
embryo, sex-mixed")
BASE COUNT      65 a      124 c      132 g      103 t
ORIGIN

Query Match      7.7%; Score 49; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTCACGAGCGCTGGGAGTCTCGACCATCGATGCTGC 458
DB 373 AGTGTGTCACGAGCGCTGGGAGTCTCGACCATCGATGCTGC 421

RESULT 4
LOCUS      BG900069      380 bp      mRNA      linear      EST 06-NOV-2001
DEFINITION HOA48-1-G2.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA
ACCESSION  BG900069
VERSION     BG900069.1 GI:14310269
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 380)
AUTHORS     Kumar,S., Connor,J.R., Dodds,R.A., Halsey,M., Van Horn,M., Mao,J.,
Sache,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-legsk.com
            Seq primer: T7.

FEATURES
    source      location/Qualifiers
                1..380
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="HOA (Human Osteoarthritic Cartilage)"
                /tissue_type="cartilage"
                /lab_host="E.coli DH10 B"
                /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
                Directional"
BASE COUNT      58 a      139 c      118 g      65 t
ORIGIN

Query Match      5.0%; Score 32; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGATGCTGCTGCTGCTG 406
DB 206 GTACCCCTGCTGATGCTGCTGCTGCTG 237

RESULT 5
LOCUS      BG900069
DEFINITION HOA51-1-A11.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
ACCESSION  BG900069
VERSION     BG900069.1 GI:14310318
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 405)
AUTHORS     Kumar,S., Connor,J.R., Dodds,R.A., Halsey,M., Van Horn,M., Mao,J.,
Sache,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-legsk.com
            Seq primer: T7.

FEATURES
    source      location/Qualifiers
                1..405
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="HOA (Human Osteoarthritic Cartilage)"
                /tissue_type="cartilage"
                /lab_host="E.coli DH10 B"
                /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
                Directional"
BASE COUNT      62 a      140 c      135 g      68 t
ORIGIN

Query Match      5.0%; Score 32; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGATGCTGCTGCTGCTG 406
DB 202 GTACCCCTGCTGATGCTGCTGCTGCTG 233

RESULT 6
LOCUS      BG538695
DEFINITION NIH-MGC http://mgi.nci.nih.gov/
ACCESSION  BG538695
VERSION     BG538695.1 GI:13530928
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 618)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LML at:
            http://image.llnl.gov

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Plate: LICM1510 row: p column: 07  
High quality sequence stop: 499.

## FEATURES

Location/Qualifiers  
1. 618

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_image="4691574"

/clone\_lib="NIH\_MGC-77"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1; SfiI (ggcgctcgccgccc); Site 2: SfiI (ggcgctcgccgccc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCGACATG-GT(30)BN-3' (where B = A, C, G or T) and N = A, C, G, or T) 3' Average insert size 1.9 kb (range 0.5-4.0 kb). 12/75 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## BASE COUNT

95 a 194 c 213 g 116 t

## Query Match

Best Local Similarity 100.0%; Score 32; DB 12; Length 618;  
Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;

## Db

375 GTACCCCTGGTGTGATGGCTGTGCTGCTG 406  
291 GTACCCCTGGTGTGATGGCTGTGCTGCTG 322

## RESULT 7

BG928868 620 bp mRNA linear EST 06-NOV-2001  
LOCUS HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
DEFINITION HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
ACCESSION BG928868  
VERSION BG928868.1 GI:14323391  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 620)  
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathie, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Cowen, M. and Lark, M.W.  
Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651

## TITLE

Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries

## JOURNAL

Medline  
Contact: Sanjay Kumar  
UM2109

## COMMENT

GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-legsk.com  
Seq primer: T7

## FEATURES

Location/Qualifiers  
1. 620

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="HNC (Human Normal Cartilage)"

/tissue\_type="cartilage"

/lab\_host="E.coli DH10 B"

/note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI; Directional"

## BASE COUNT

97 a 218 c 207 g 98 t

## Query Match

5.0%; Score 32; DB 13; Length 620;

Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGGTGTGATGGCTGTGCTGCTG 406  
Db 210 GTACCCCTGGTGTGATGGCTGTGCTGCTG 241

## RESULT 8

BI457141 651 bp mRNA linear EST 21-AUG-2001  
LOCUS BI457141  
DEFINITION 603185392F1 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:5258159 5', mRNA sequence.

## ACCESSION

BI457141  
BI457141.1 GI:15247797

## VERSION

EST.

## KEYWORDS

human.

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 651)  
NIH-MGC <http://mgs.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: Ling Hong/Rubin Laboratory (LLNL)  
DNA Sequencing by: Inocyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LICM1869 row: g column: 24  
High quality sequence stop: 651.

## FEATURES

Location/Qualifiers  
1. 651

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_image="5258159"

/clone\_lib="NIH\_MGC-42"

/tissue\_type="epitheloid carcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pDNR; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## BASE COUNT

91 a 230 c 219 g 111 t

## Query Match

5.0%; Score 32; DB 13; Length 651;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Db

375 GTACCCCTGGTGTGATGGCTGTGCTGCTG 406  
96 GTACCCCTGGTGTGATGGCTGTGCTGCTG 127

## RESULT 9

AL555144 749 bp mRNA linear EST 16-FEB-2001  
LOCUS AL555144 LIT\_NFL006-PL2 Homo sapiens cDNA clone CS0DK007021 5  
DEFINITION AL555144 LIT\_NFL006-PL2 Homo sapiens cDNA clone CS0DK007021 5  
ACCESSION AL555144  
VERSION AL555144.1 GI:12896595  
KEYWORDS EST.  
SOURCE human.

## BASE COUNT

97 a 218 c 207 g 98 t

## Query Match

5.0%; Score 32; DB 13; Length 620;

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 749)  
Li, M.B., Gruber, C., Jessee, J. and Polayres, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

Source

1..749  
Location/Qualifiers

BASE COUNT

128 a 252 c 236 g 133 t

ORIGIN

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

375 GTACCCCTGTCGTGATGCTGCTGCTG 406  
|||||  
432 GTACCCCTGTCGTGATGCTGCTGCTG 463

RESULT 10

BM043988 750 bp mRNA linear EST 07-NOV-2001

LOCUS

60362097BP1 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:5446794 5',  
mRNA sequence.

ACCESSION

BM043988  
EST.  
BM043988.1 GI:16773255

VERSION

EST.

KEYWORDS

human.

SOURCE

human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 750)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM1929 row: k column: 19  
High quality sequence stop: 714.

FEATURES

Source

1..750  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5446794"  
/clone\_lib="NIH\_MGC\_40"

/tissue\_type="carcinoma, cell line"  
/db\_host="DH10B (phage-resistant)"  
/note="Organ: prostate; Vector: pOT7; Site:1: XhoI;  
Site:2: EcoRI. cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GCCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT

112 a 267 c 246 g 125 t

ORIGIN

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

375 GTACCCCTGTCGTGATGCTGCTGCTG 406  
|||||  
142 GTACCCCTGTCGTGATGCTGCTGCTG 173

Db

RESULT 11

B1826781 800 bp mRNA linear EST 04-OCT-2001

LOCUS

60307726BP1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5169065 5',  
mRNA sequence.

ACCESSION

B1826781  
EST.  
B1826781.1 GI:15938331

VERSION

EST.

KEYWORDS

human.

SOURCE

human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 800)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LRAM1420 row: g column: 18  
High quality sequence stop: 788.

FEATURES

Source

1..800  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5169065"  
/clone\_lib="NIH\_MGC\_119"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;  
Site:2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

BASE COUNT

115 a 284 c 264 g 136 t 1 others

ORIGIN

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258398"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
Site: 2; EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library. 1"

BASE COUNT      136 a      305 c      304 g      170 t      1 others
ORIGIN

Query Match      5.0%; Score 32; DB 13; Length 916;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      375 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 406
      |||||||
Db      96 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 127

RESULT 15
BI161474      928 bp      mRNA      linear      EST 05-JUL-2001
LOCUS      602864871f1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019065 5',
DEFINITION      mRNA sequence.
ACCESSION      BI161474
VERSION      BI161474.1 GI:14621475
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 928)
AUTHORS      NIH-MGC http://mgc.ncl.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs@email.nih.gov
      Tissue Procurement: ATCC.
      cDNA Library Preparation: Ling Hong/Rubin Laboratory
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.llnl.gov
      Plate: L10M183 row: m column: 18
      High quality sequence start: 28
      High quality sequence stop: 756.
      Location/Qualifiers
        1..928
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /clone="IMAGE:5019065"
          /clone_lib="NIH_MGC_42"
          /tissue_type="epithelioid carcinoma cell line"
          /lab_host="DH10B (phage-resistant)"
          /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
          Site: 2; EcoRI; cDNA made by oligo-dT priming.
          directionally cloned into EcoRI/XhoI sites using the
          following 5' adaptor: GGCACGAG(G). Size-selected >500bp
          for average insert size 1.8kb. Library constructed by Ling
          Hong in the laboratory of Gerald M. Rubin (University of
          California, Berkeley) using ZAP-cDNA synthesis kit
          (Stratagene) and Superscript II RT (Life Technologies).
          Note: this is a NIH_MGC library. 1"

BASE COUNT      161 a      301 c      309 g      157 t
```

```
ORIGIN

Query Match      5.0%; Score 32; DB 13; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      375 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 406
      |||||||
Db      188 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 219

Search completed: July 28, 2003, 18:02:05
Job time : 1127.46 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:19:16 ; Search time 2453.86 Seconds

(without alignments)  
10472.371 Million cell updates/sec

Title: US-10-010-408-1\_COPY\_1\_883

Perfect score: 883  
Sequence: 1 GACGCTCTGATCTCCAGAG.....ACCACCTGTGGCTGGGCAT 883Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	218	24.7	137964	2	AC126895	AC126895 Rattus no
2	218	24.7	226303	2	AC095418	AC095418 Rattus no
3	166	18.8	137964	2	AC126895	AC126895 Rattus no
4	117	13.3	1741	10	AF259981	AF259981 Rattus no
5	90	10.2	1734	6	AR210324	AR210324 Sequence
6	90	10.2	1734	6	AR210325	AR210325 Sequence
7	90	10.2	1734	10	AF100778	AF100778 Mus muscu
8	90	10.2	61072	10	AL731698	AL731698 Mus muscu
9	90	10.2	216757	2	AL669906	AL669906 Mus muscu
10	80	9.1	1739	10	AF126063	AF126063 Mus muscu
11	32	3.6	738	6	AR210337	AR210337 Sequence
12	32	3.6	841	6	AR210338	AR210338 Sequence
13	32	3.6	1266	6	AX076919	AX076919 Sequence
14	32	3.6	1266	6	AX464186	AX464186 Sequence
15	32	3.6	1283	6	AF083500	AF083500 Homo sapi
16	32	3.6	1293	6	AR210322	AR210322 Sequence
17	32	3.6	1293	6	AR210323	AR210323 Sequence
18	32	3.6	1309	9	AF074604	AF074604 Homo sapi
19	32	3.6	1427	9	AF100780	AF100780 Homo sapi
20	32	3.6	1450	9	BC017782	BC017782 Homo sapi
21	32	3.6	107260	9	AL139352	AL139352 Human DNA
22	27	3.1	51	6	AR210371	AR210371 Sequence
23	27	3.1	51	6	AX076923	AX076923 Sequence
24	22	2.5	99395	5	AC010446	AC010446 Homo sapi
25	22	2.5	142142	2	AC091173	AC091173 Homo sapi
26	22	2.5	149483	2	AC110904	AC110904 Mus muscu
27	22	2.5	180464	2	AC116351	AC116351 Homo sapi
28	22	2.5	186676	9	AC067881	AC067881 Homo sapi
29	22	2.5	200050	1	AL646068	AL646068 Ralstonia
30	21	2.4	66908	2	AC119914	AC119914 Mus muscu
31	21	2.4	150944	2	AC112856	AC112856 Rattus no
32	21	2.4	134881	2	AC122102	AC122102 Rattus no
33	21	2.4	181343	10	AL671882	AL671882 Mouse DNA
34	21	2.4	204937	2	AL831741	AL831741 Mus muscu
35	21	2.4	215105	2	AC073717	AC073717 Mus muscu
36	20	2.3	1003	5	CHRTCEAA	M73064 Chicken T-c
37	20	2.3	1200	6	AX122384	AX122384 Sequence
38	20	2.3	1221	9	HS8001506	AL133637 Homo sapi
39	20	2.3	1481	8	AB033535	AB033535 Oryza sat
40	20	2.3	3301	9	BC019257	BC019257 Homo sapi
41	20	2.3	4467	9	AB020659	AB020659 Homo sapi
42	20	2.3	7172	10	AB008516	AB008516 Mus muscu
43	20	2.3	36296	9	HS8159	Z82180 Human DNA s
44	20	2.3	83021	2	AC095541	AC095541 Rattus no
45	20	2.3	84001	9	AL162739	AL162739 Human DNA

## ALIGNMENTS

RESULT 1  
AC126895  
LOCUS  
DEFINITION  
AC126895 137964 bp DNA linear HTG 24-JUL-2002  
Rattus norvegicus clone CH230-301E4, \*\*\* SEQUENCING IN PROGRESS  
\*\*\* 49 unordered pieces.  
AC126895  
AC126895.1 GI:21724040  
VERSION  
KEYWORDS  
HTG: HTGS\_PHASE1.  
SOURCE  
Rattus norvegicus  
ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE  
1 (bases 1 to 137964)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,

Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayele, M., Banks, T.,  
 Barbieri, J., Benton, J., Bimaga, K., Blankenburg, K., Bonin, D.,  
 Bouck, J., Bowle, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,  
 Buha, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,  
 Carion, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chaver, D.,  
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,  
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,  
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 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,  
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durkin, K.J.,  
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 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P.,  
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 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,  
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 Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,  
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,  
 Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K.,  
 Wu, C., Wu, X., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
 Welnsstock, G., and Gibbs, R.

Unpublished  
 Direct Submission  
 2 (bases 1 to 137964)  
 Morley, K.C.

Direct Submission  
 Submitted (10-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 137964)  
 Morley, K.C.

Direct Submission  
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GZHG  
 Center clone name: CH230-301E4  
 ----- Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 89474 bases at least Q40  
 Consensus quality: 93423 bases at least Q30  
 Consensus quality: 96506 bases at least Q20

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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 49 contigs. The true order of the pieces

\* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1  
 1057  
 1157  
 2336  
 2436  
 3443  
 3543  
 5082  
 5181  
 6425  
 6525  
 7815  
 7915  
 9154  
 9254  
 10446  
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 2335: contig of 1179 bp in length  
 2435: gap of unknown length  
 3442: contig of 1007 bp in length  
 3542: gap of unknown length  
 5081: contig of 1533 bp in length  
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 7814: contig of 1290 bp in length  
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 9153: contig of 1233 bp in length  
 9253: gap of unknown length  
 10445: contig of 1192 bp in length  
 10545: gap of unknown length  
 11771: contig of 1226 bp in length  
 11871: gap of unknown length  
 13240: contig of 1369 bp in length  
 13340: gap of unknown length  
 14359: contig of 1019 bp in length  
 14459: gap of unknown length  
 15551: contig of 1192 bp in length  
 15751: gap of unknown length  
 17494: contig of 1743 bp in length  
 17594: gap of unknown length  
 18679: contig of 1085 bp in length  
 18779: gap of unknown length  
 20681: contig of 1902 bp in length  
 20781: gap of unknown length  
 22118: contig of 1337 bp in length  
 22218: gap of unknown length  
 23578: contig of 1360 bp in length  
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 25423: contig of 1745 bp in length  
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 30272: contig of 2364 bp in length  
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 33191: gap of unknown length  
 35777: contig of 2586 bp in length  
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 36908: contig of 1031 bp in length  
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 38930: contig of 1922 bp in length  
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 50433: contig of 2116 bp in length  
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 53194: contig of 2214 bp in length  
 55294: gap of unknown length  
 57482: contig of 2188 bp in length  
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 60781: contig of 3199 bp in length  
 60881: gap of unknown length  
 62599: contig of 1718 bp in length

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* 62600 62699: gap of unknown length
* 62700 65203: contig of 2504 bp in length
* 65204 65303: gap of unknown length
* 65304 65914: contig of 1611 bp in length
* 65915 67014: gap of unknown length
* 67015 70839: contig of 3825 bp in length
* 70840 70940 75139: gap of unknown length
* 70940 75139: contig of 4200 bp in length
* 75140 75239: gap of unknown length
* 75240 78296: contig of 3057 bp in length
* 78297 78396: gap of unknown length
* 78397 83138: contig of 4742 bp in length
* 83139 83338: gap of unknown length
* 83239 88204: contig of 4966 bp in length
* 88205 92238: gap of unknown length
* 92239 92338: contig of 3934 bp in length
* 92339 97339: gap of unknown length
* 97340 97439: gap of 5001 bp in length
* 97440 103534: contig of 6095 bp in length
* 103535 103634: gap of unknown length
* 103635 107080: contig of 3446 bp in length
* 107081 107180: gap of unknown length
* 107181 115201: contig of 8021 bp in length
* 115202 115301: gap of unknown length
* 115302 121337: contig of 5936 bp in length
* 121338 121337: gap of unknown length
* 121338 127910: contig of 6573 bp in length
* 127911 128010: gap of unknown length
* 128011 137964: contig of 9954 bp in length.
Location/Qualifiers
1. 137964
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-7C10"

```

```

BASE COUNT 31831 a 34027 c 35229 g 31979 t 4898 others
ORIGIN

```

```

Query Match 24.7%: Score 218; DB 2; Length 137964;
Best Local Similarity 100.0%; Pred. No. 2,1e-105;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 308 GGTGTGTGCTCCAGCTGTGCGGACACCTGTACCTGTCTTGACACCAACCCAGTGGCC 367
DB 104664 GGTGTGTGCTCCAGCTGTGCGGACACCTGTACCTGTCTTGACACCAACCCAGTGGCC 104723
OY 368 ACAGGGGGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
DB 104724 ACAGGGGGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 104783
OY 428 TGGGGAGTCTCTGCGACACCTGTACCTGTGCGGACCCAGGGGCTGCTGCTGCTGCTGCTGCT 487
DB 104784 TGGGGAGTCTCTGCGACACCTGTACCTGTGCGGACCCAGGGGCTGCTGCTGCTGCTGCTGCT 104843
OY 488 TGGGGAGTCTCTGCGACACCTGTACCTGTGCGGACCCAGGGGCTGCTGCTGCTGCTGCTGCT 525
DB 104844 TGGGGAGTCTCTGCGACACCTGTACCTGTGCGGACCCAGGGGCTGCTGCTGCTGCTGCTGCT 104881

```

```

RESULT 2
AC095418 226303 bp DNA linear HTG 11-JUL-2002
LOCUS Rattus norvegicus clone CH230-7C10, *** SEQUENCING IN PROGRESS ***
DEFINITION 51 unnumbered pieces.
AC095418
AC095418.3 GI:21717893
VERSION HTG; HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 226303)

```

## AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albrooks, S.L., Amaralunge, H.C., Are, J.R., Ayale, M., Banks, T., Barbarta, J., Benton, J., Blmage, K., Blankenburg, K., Bonnin, D., Bouck, J., Boyle, S., Bileva, M., Brown, E., Brown, M., Bryant, N.P., Bunay, C., Burch, P., Burkelt, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hughes, M., Holloway, C., Hollins, B., Homsl, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jollivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Krstovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Louised, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mashiney, E., Mcleod, M.P., Meador, M., Mei, G., Metzger, M., Mier, G., Mier, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nkokenko, S., Ogun, M., Okunnu, G., Orengue, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatek, A., Tabor, P., Tameisa, A., Tameisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tellard, B., Thomas, R., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalton, D., Vinsom, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleceyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Glbbs, R.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

## COMMENT

Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
(bases 1 to 226303)  
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 10, 2002 this sequence version replaced gi:17941885.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GCDF  
Center clone name: CH230-7C10  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye: 100% of reads  
Assembly program: Phrap: version 0.990329  
Consensus quality: 185950 bases at least Q40  
Consensus quality: 190362 bases at least Q30  
Consensus quality: 193076 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).



## ORGANISM

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
AUTHORS

1 (bases 1 to 137964)

Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C.,  
Albrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,  
Bardaraj,J., Benton,J., Blinag,K., Bonlath,D., Bonlath,D.,  
Bouck,J., Bowe,S., Brileva,M., Brown,E., Brown,N., Bryant,N.P.,  
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,  
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
Devalla,M.L., Davis,C., Davy-Carroll,L., Dederich,A.,  
Dejaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,  
Douthett,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,  
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,  
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,  
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,  
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Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,  
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,  
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,  
Krivoyac,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
Li,J., Li,Z., Lichteberg,O., Lieu,C., Liu,J., Liu,W., Louisedge,H.,  
Locado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,  
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metker,M.,  
Meyer,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,  
Mosier,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okunolu,G.,  
Orquyue,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,  
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Rivers,M., Rojas,A., Rojokokan,I., Rolfe,M., Ruiz,S., Savary,G.,  
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,  
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Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,  
Usmani,K., Vasquez,L., Vera,Y., Villalon,D., Vinson,R., Wang,Q.,  
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,K.,  
Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 137964)

Worley,K.C.

Direct Submission

Submitted (10-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 137964)

Worley,K.C.

Direct Submission

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

## COMMENT

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: G2HG

Center clone name: CH230-301E4

----- Summary Statistics

Sequencing vector: Plasmid:

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: Version 0.990329

Consensus quality: 894/74 bases at least Q40

Consensus quality: 934/22 bases at least Q30

Consensus quality: 96506 bases at least Q20

-----  
\* NOTE: Estimated insert size may differ from sequence length.  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_drift\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_drift_data.html)).  
\* NOTE: This is a working draft sequence. It currently  
\* consists of 49 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
1056: contig of 1056 bp in length  
1057  
1156: gap of unknown length  
1157  
2335: contig of 1179 bp in length  
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3442: contig of 1007 bp in length  
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3542: gap of unknown length  
3543  
5081: contig of 1539 bp in length  
5082  
5181: gap of unknown length  
5182  
6424: contig of 1243 bp in length  
6425  
6524: gap of unknown length  
6525  
7814: contig of 1290 bp in length  
7914: gap of unknown length  
9153: contig of 1239 bp in length  
9154  
9253: gap of unknown length  
9254  
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10446  
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17594: gap of unknown length  
18679: contig of 1085 bp in length  
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22118: gap of unknown length  
22119  
23578: contig of 1360 bp in length  
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23678: gap of unknown length  
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25423: contig of 1745 bp in length  
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25523: gap of unknown length  
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33191: gap of unknown length  
35777: contig of 2586 bp in length  
35778  
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41210: contig of 2180 bp in length  
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41310: gap of unknown length  
41311  
42937: contig of 1627 bp in length  
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46220: gap of unknown length  
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50534  
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52981  
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*	57483	57882: gap of unknown length
*	57583	60781: contig of 3199 bp in length
*	60782	60881: gap of unknown length
*	60882	62929: contig of 1718 bp in length
*	62600	62699: gap of unknown length
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*	65204	65503: gap of unknown length
*	65304	66914: contig of 1611 bp in length
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*	67015	70839: contig of 3825 bp in length
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*	75140	75239: gap of unknown length
*	75240	78296: contig of 3057 bp in length
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*	103635	107080: contig of 3446 bp in length
*	107081	107180: gap of unknown length
*	107181	115201: contig of 8021 bp in length
*	115202	115301: gap of unknown length
*	115302	121237: contig of 5936 bp in length
*	121238	121337: gap of unknown length
*	121338	127910: contig of 6573 bp in length
*	127911	128010: gap of unknown length
*	128011	137964: contig of 9954 bp in length

	a	c	g	t	others
BASE COUNT	31831	34027	35229	31979	4898
ORIGIN					

Query Match	18.8%	Score 166;	DB 2;	Length 137964;
Best Local Similarity	99.5%	Pred. No. 1.3e-77;		
Matches 216;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0

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Db	74321	GAGCGTTCTGATATCTCCAGAGGACCCCTGGGGTGGGACAGGGGCCCTTGGCAAGGCTGCAGCC	74262
QY	61	GCTGGGCAAGTGGCTTGGAAATGAGAGTCTTTATTAAGTGGGAACTGAGAGACTTAAGAGCTTC	120
Db	74261	GCTGGGCAAGTGGCTTGGAAATGAGAGTCTTTATTAAGTGGGAACTGAGAGACTTAAGAGCTTC	74202
QY	121	CTGTCAAGCTTGTCTTAAAGTCTTTAGACATTTGGTGGCTTGGGGCTTACACACTGTGACA	180
Db	74201	CTGTCAAGCTTGTCTTAAAGTCTTTAGACATTTGGTGGCTTGGGGCTTACACACTGTGACA	74142
QY	181	CACCTTCGTGGTGGCTCCACAGGCGCTCACCTTTCAGGT	217
Db	74141	CACCTTCGTGGTGGCTCCACAGGCGCTCACCTTTCAGGT	74105

RESULT 4	AF259981	1741 bp	RNA	linear	ROD 09-MAY-2000
LOCUS	AF259981				
DEFINITION	Rattus norvegicus CCN family protein COP-1 (COP-1) mRNA, complete cds.				
ACCESSION	AF259981				
VERSION	AF259981.1	GI:7739780			
KEYWORDS					

SOURCE	Rattus norvegicus .
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 1741)
AUTHORS	Zhang, R., Averboukh, L., Zhu, W., Zhang, H., Jo, H., Dempsey, P. J., Coffey, R. J., Pardoe, A. B. and Liang, P.
TITLE	Identification of rCop-1, a new member of the CCN protein family, as a negative regulator for cell transformation
JOURNAL	Mol. Cell. Biol. 18 (10), 6131-6141 (1998)
MEDLINE	98414629
PUBMED	9742130
REFERENCE	2 (bases 1 to 1741)
AUTHORS	Liang, P.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer Center, 649 MRB II, Nashville, TN 37232, USA
FEATURES	Location/Qualifiers
SOURCE	1..1741

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CDS

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262. .1014  
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BASE COUNT  
BRGIN

386 a 491 c 480 g 364 t

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Best Local Similarity	99.1%	Pred. No. 5.1e-51		
Matches 217	Conservative 0	Mismatches 2	Indels 0	Gaps 0

Dy  
665 GCGTCCCAAGCTGGGACTGTGCCACAGCCCCAAGAGATATTACAGGTGCCAGGAAGAAGTGTCGCC 724

Dd  
678 GCATGCCCAAGCTGGGACTGTGCCACAGCCCCAAGAGATATTACAGGTGCCAGGAAGAAGTGTCGCC 737

QY	725	CGAATGGGTATGTATGACCAAGGAGTGTACACCGGCATCCAGGGCTTCACAGGGCGCAAGAGCA	784
Db	738	CGAATGGGTATGTATGACCAAGGAGTGTACACCGGCATCCAGGGCTTCAGGGCGCGCAAGAGCA	797
QY	785	CCAACTTTCGCGCCCTTGTCATCCCTGCGCTCGTGCATGCTCCTGTCCAAATTGGAGAGC	844
Db	798	CCAACTTTCGCGCCCTTGTCATCCCTGCGCTCGTGCATGCTCCTGTGGCCAAATTGGAGAGC	857
QY	845	AGCCTGGGGCCCTGCTCTCAACCACTGTGGGCTGGGCAT	883
Db	858	AGCCTGGGGCCCTGCTCTCAACCACTGTGGGCTGGGCAT	896

RESULT	5
LOCUS	AR210324
DEFINITION	AR210324
ACCESSION	Sequence 17 from patent US 6387657.
VERSION	AR210324
KEYWORDS	AR210324.1 GI:21512525
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1734) Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M Ann. and Wood,W.T.

TITLE WISP polypeptides and nucleic acids encoding same  
JOURNAL Patent: US 6387657-A 17 14-MAY-2002;  
FEATURES Location/Qualifiers  
source 1..1734  
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BASE COUNT 355 a 491 c 495 g 393 t

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Best Local Similarity 100.0%; Pred. No. 1.4e-36;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGTGCACGAGAGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCCA 469  
|||||  
DB 418 AGTGTGTGCACGAGAGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCCA 477  
OY 470 GGGCCTGGTTGTGCAGCCTGGGGAGGCC 499  
|||||  
DB 478 GGGCCTGGTTGTGCAGCCTGGGGAGGCC 507

RESULT 6  
AR210325/c 1734 bp DNA linear PAT 20-JUN-2002  
LOCUS Sequence 18 from patent US 6387657.  
ACCESSION AR210325  
VERSION AR210325.1 GI:21512526  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1734)  
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,  
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.  
TITLE WISP polypeptides and nucleic acids encoding same  
JOURNAL Patent: US 6387657-A 18 14-MAY-2002;  
FEATURES Location/Qualifiers  
source 1..1734  
/organism="unknown"

BASE COUNT 393 a 495 c 491 g 355 t

Query Match 10.2%; Score 90; DB 6; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.4e-36;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGTGCACGAGAGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCCA 469  
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DB 1317 AGTGTGTGCACGAGAGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCCA 1258  
OY 470 GGGCCTGGTTGTGCAGCCTGGGGAGGCC 499  
|||||  
DB 1257 GGGCCTGGTTGTGCAGCCTGGGGAGGCC 1228

RESULT 7  
AF100778 1734 bp mRNA linear ROD 17-DEC-1998  
LOCUS Mus musculus connective tissue growth factor related protein WISP-2  
DEFINITION (WISP2) mRNA, complete cds.  
ACCESSION AF100778  
VERSION AF100778.1 GI:4028578  
KEYWORDS  
SOURCE Mus musculus.  
ORGANISM Mus musculus.  
REFERENCE 1 (bases 1 to 1734)  
AUTHORS Pennica,D., Swanson,T.A., Welsh,J.W., Roy,M.A., Lawrence,D.A.,  
Lee,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., Matanabe,C.,  
Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D.,  
Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J.  
TITLE WISP genes are members of the connective tissue growth factor

JOURNAL family that are up-regulated in wt1-transformed cells and  
MEDLINE aberrantly expressed in human colon tumors  
99061933  
PUBMED 9843955  
REFERENCE 2 (bases 1 to 1734)  
AUTHORS Pennica,D.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-1998) Molecular Oncology, Genentech, Inc., 1 DNA  
Way, South San Francisco, CA 94080, USA  
FEATURES Location/Qualifiers  
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WVCDQAVWQPAIOPSSAOGHLSALVPAADGCPNMWSTWAGPCSTTCGLIATRV  
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BASE COUNT 355 a 491 c 495 g 393 t

Query Match 10.2%; Score 90; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.4e-36;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGTGCACGAGAGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCCA 469  
|||||  
DB 418 AGTGTGTGCACGAGAGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCCA 477  
OY 470 GGGCCTGGTTGTGCAGCCTGGGGAGGCC 499  
|||||  
DB 478 GGGCCTGGTTGTGCAGCCTGGGGAGGCC 507

RESULT 8  
AL731698 61072 bp DNA linear ROD 24-MAY-2002  
LOCUS Mouse DNA sequence from clone Rp23-161B3 on chromosome 2, complete  
DEFINITION sequence.  
ACCESSION AL731698  
VERSION AL731698.10 GI:21214309  
KEYWORDS HTG.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE 1 (bases 1 to 61072)  
AUTHORS Wallis,J.  
TITLE Direct Submission  
JOURNAL Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On May 25, 2002 this sequence version replaced gi:21213601.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone, and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at <http://www.sanger.ac.uk/projects/C.elegans/wormpep> RP23-161B3 is from the RP23 Mouse PAC library constructed by the group of Pletier de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6.

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BASE COUNT 15405 a 15368 c 15033 g 15266 t

## ORIGIN

Query Match 10.2%; Score 90; DB 10; length 61072;  
Best Local Similarity 100.0%; Pred. No. 7.1e-37;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10029 AGGTGTGCACGAGAGCTGGGAGATCTGCGACACCTGCATGTCGACCCAGCCA 10088

QY 470 GGCCCTGTTTTCAGCTGGGAGAGCC 499

Db 10089 GGCCCTGTTTTCAGCTGGGAGAGCC 10118

RESULT 9  
AL669906 216757 bp DNA linear HTG 24-JUL-2002

LOCUS AL669906 chromosome 2 clone RP23-217C2, \*\*\* SEQUENCING IN

DEFINITION PROGRESS \*\*\*, 21 unordered pieces.

ACCESSION AL669906 GI:21955520

VERSION AL669906.5 HTG: HTGS\_PHASE1; HTGS\_CANCELLED.

KEYWORDS Mus musculus.

SOURCE Mus musculus.

ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 216757)

TITLE Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,

JOURNAL Cambridgehire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

COMMENT On Jul 25, 2002 this sequence version replaced gi:18181793.

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: [humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk)

Project Information

Center project name: bm217C2

Summary Statistics:

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 211865 bases at least 940

Consensus quality: 213403 bases at least 930

Consensus quality: 214139 bases at least 920

Insert size: 214757; sum-of-contigs

Insert size: 234243; 1.88 error; agarose-fp

Quality coverage: 6.29x in 920 bases; sum-of-contigs Quality coverage: 5.90x in 920 bases; agarose-fp

\*\*\*\*\*  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 21 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
4001 4100: contig of 4000 bp in length  
4101 15267: contig of 11167 bp in length  
15268 15367: gap of 100 bp  
15368 34970: contig of 19603 bp in length  
34971 35070: gap of 100 bp  
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39672 39771: gap of 100 bp  
39772 46360: contig of 6589 bp in length  
46361 46460: gap of 100 bp  
46461 49809: contig of 3349 bp in length  
49810 49909: gap of 100 bp  
49910 54509: contig of 4600 bp in length  
54510 54609: gap of 100 bp  
54610 65989: contig of 11380 bp in length  
65990 66089: gap of 100 bp  
66090 84635: contig of 18546 bp in length  
84636 84735: gap of 100 bp  
84736 87399: contig of 2664 bp in length  
87400 87499: gap of 100 bp  
87500 98601: contig of 11102 bp in length  
98602 98701: gap of 100 bp  
98702 105522: contig of 6821 bp in length  
105523 105622: gap of 100 bp  
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119774 119873: gap of 100 bp  
119874 134552: contig of 14679 bp in length  
134553 134652: gap of 100 bp  
134653 141202: contig of 6550 bp in length  
141203 141302: gap of 100 bp  
141303 145808: contig of 4506 bp in length  
145809 145908: gap of 100 bp  
145909 151572: contig of 5664 bp in length  
151573 151672: gap of 100 bp  
151673 169686: contig of 18014 bp in length  
169687 169786: gap of 100 bp  
169787 200095: contig of 30309 bp in length  
200096 200195: gap of 100 bp  
200196 213877: contig of 13682 bp in length  
213878 213977: gap of 100 bp  
213978 216757: contig of 2780 bp in length.

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Best Local Similarity 100.0%; Pred. No. 5.6e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 410 AGTGTGTCACGAGGCTGGGGAGTCTCTGCAGCACCTGTCATGTCTGCGAGCCAGCCA 469
DB 166450 AGTGTGTCACGAGGCTGGGGAGTCTCTGCAGCACCTGTCATGTCTGCGAGCCAGCCA 166509
QY 470 GGGCGCTGGTTGTCACTCGGGGCGAGGCC 499
DB 166510 GGGCGCTGGTTGTCACTCGGGGCGAGGCC 166539
RESULT 10
AF126063 1739 bp mRNA linear ROD 12-OCT-1999
DEFINITION Mus musculus connective tissue growth factor-like protein precursor
(Ctgfl) mRNA, complete cds.
ACCESSION AF126063

```

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VERSION AF126063.1 GI:4337059
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 1739)
AUTHORS Kumar,S., Hand,A.T., Connor,J.R., Dodds,R.A., Ryan,P.J.,
Trill,J.J., Fisher,S.M., Nuttall,M.E., Lipshutz,D.B., Zou,C.,
Hwang,S.M., Volta,B.J., James,I.E., Rileman,D.J., Gowen,M. and
Lee,J.C.
TITLE Identification and cloning of a connective tissue growth
factor-like cDNA from human osteoblasts encoding a novel regulator
of osteoblast functions
JOURNAL J. Biol. Chem. 274 (24), 17123-17131 (1999)
MEDLINE 99287915
PUBMED 10358067
REFERENCE 2 (bases 1 to 1739)
AUTHORS Kumar,S. and Zou,C.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1999) Bone & Cartilage Biology, UW 2109,
SmithKline Beecham, 709 Swedeland Rd., King of Prussia, PA 19406,
USA
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="Lung"
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242..997
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and thrombospondin type I (TSP1) domains; member of the
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Best Local Similarity 100.0%; Pred. No. 3.2e-31;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 420 CGAGGCTGGGGAGTCTCTGCAGCACCTGCATGTCTCGAGCCAGCGCTGTT 479
DB 413 CGAGGCTGGGGAGTCTCTGCAGCACCTGCATGTCTCGAGCCAGCGCTGTT 472
QY 480 TGTCAAGCTGGGGCGAGGCC 499
DB 473 TGTCAAGCTGGGGCGAGGCC 492
RESULT 11
AR210337 738 bp DNA linear PAT 20-JUN-2002
LOCUS AR210337
DEFINITION Sequence 38 from patent US 6387657.
ACCESSION AR210337
VERSION AR210337.1 GI:21512542
KEYWORDS

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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 738)  
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.  
TITLE WISP polypeptides and nucleic acids encoding same  
JOURNAL Patent: US 6387657-A 38 14-MAY-2002;  
FEATURES  
source 1..738  
Location/Qualifiers  
/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGGTGTGGATGGCTGTGGCTGTG 406  
Db 115 GTACCCCTGGTGTGGATGGCTGTGGCTGTG 146  
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RESULT 12  
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LOCUS Sequence 39 from patent US 6387657.  
DEFINITION AR210338  
ACCESSION AR210338  
VERSION AR210338.1 GI:21512543  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 841)  
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.  
TITLE WISP polypeptides and nucleic acids encoding same  
JOURNAL Patent: US 6387657-A 39 14-MAY-2002;  
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source 1..841  
Location/Qualifiers  
/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GAGGATGCGGCTGCCACGCTGGGACTGCC 685  
Db 417 GAGGATGCGGCTGCCACGCTGGGACTGCC 448  
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RESULT 13  
AX076919 1266 bp DNA linear PAT 22-FEB-2001  
LOCUS Sequence 31 from Patent WO0105836.  
DEFINITION AX076919  
ACCESSION AX076919  
VERSION AX076919.1 GI:13121575  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and Wood,W.I.  
TITLE Polypeptide compositions and methods for the treatment of tumors  
JOURNAL Patent: WO 0105836-A 31 25-JAN-2001;  
FEATURES  
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Location/Qualifiers  
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BASE COUNT 216 a 418 c 390 g 242 t  
ORIGIN /db\_xref="taxon:9606"

Query Match 3.6%; Score 32; DB 6; Length 1266;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
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Db- 136 GTACCCCTGGTGTGGATGGCTGTGGCTGTG 167  
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RESULT 14  
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LOCUS Sequence 319 from Patent WO0140466.  
DEFINITION AX464186  
ACCESSION AX464186  
VERSION AX464186.1 GI:21899109  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Flivartoff,E., Gao,W.Q., Gerlitsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same  
JOURNAL Patent: WO 0140466-A 319 07-JUN-2001;  
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Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Homo sapiens connective tissue growth factor-like protein  
DEFINITION AF083500  
ACCESSION AF083500  
VERSION AF083500.1 GI:3462835  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Kumar,S., Hand,A.T., Connor,J.C., Dadds,R.A., Ryan,P.J., Trill,J.G., Fisher,S.M., Slemmon,D.R., Lipschutz,D.B., Bartholomew,V., James,I.E., Rleman,D.J., Gowen,M. and Lee,J.C.  
TITLE novel cysteine rich protein containing an IGF binding domain  
JOURNAL Bone 23 (5), S240 (1998)  
REFERENCE 2 (bases 1 to 1283)  
AUTHORS Kumar,S.  
TITLE Direct Submission  
JOURNAL Submitted (11-AUG-1998) Bone & Cartilage Biology, UM 2109, Smithkline Beecham, 709 Swedeland Road, King Of Prussia, PA 19406,

FEATURES USA

Location/Qualifiers  
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/db\_xref="taxon:9606"  
/chromosome="20"  
/map="20q12-q13"  
/cell\_type="primary osteoblast"  
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/db\_xref="GI:3462836"  
/translation="MRGTPKTHLAFSLILCLLSKVRQLCPTPCPCMPPPRCPLGVP  
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NGRLYREGTEFOPHCSTRCEODGFTVCPLCSFDVRLPSMDCHPRRREVLKCCPE  
MYCGGGGLGTQPLPAOGPQPSGLVSSLPGVPCPEWSTAMGPCSTTCGLGMATRVSN  
QNRCRLETRRLCLSRCPSPSRGRSPNSAF"

CDS  
BASE COUNT 235 a 418 c 389 g 241 t  
ORIGIN

Query Match 3.6%; Score 32; DB 9; Length 1283;  
Best Local Similarity .100.0%; Pred. No. 1.0e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 135 GTACCCCTGGTGTGATGGCTGTGCTGCTG 166

Search completed: July 28, 2003, 21:14:41  
Job time : 2455.86 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:31:11 ; Search time 231.91 seconds  
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8574.520 Million cell updates/sec

Title: US-10-010-408-1\_COPY\_1\_883

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Scoring table:

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Searched: 2185239 seqs, 112599159 residues

Word size: 0

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	883	100.0	1708	20	AAZ07516
2	635	71.9	753	20	AAZ07517
3	566	64.1	681	20	AAZ07521
4	210	23.8	210	20	AAZ07519
5	177	20.0	177	20	AAZ07518
6	90	10.2	753	20	AAZ07518
7	90	10.2	1734	20	AAZ07518
8	59	6.7	174	20	AAZ07520
9	32	3.6	199	22	ABA72245

10	32	3.6	199	22	ABA38112
11	32	3.6	199	22	AAK20667
12	32	3.6	199	22	AAK46811
13	32	3.6	199	22	AAI25749
14	32	3.6	199	22	AAI25650
15	32	3.6	199	24	AB521124
16	32	3.6	586	22	ABA50703
17	32	3.6	586	22	ABA28232
18	32	3.6	586	22	AAK07972
19	32	3.6	586	22	AAK33842
20	32	3.6	586	22	AAI16552
21	32	3.6	586	22	AAI39568
22	32	3.6	586	24	AB508689
23	32	3.6	738	20	AAZ07501
24	32	3.6	750	20	AAZ07501
25	32	3.6	841	20	AAZ07502
26	32	3.6	1257	20	AAZ07502
27	32	3.6	1266	21	AAA30048
28	32	3.6	1266	22	AAZ07503
29	32	3.6	1266	22	AAZ07503
30	32	3.6	1266	22	AAZ07503
31	32	3.6	1266	22	AAZ07503
32	32	3.6	1267	21	AAZ07506
33	32	3.6	1285	19	AAZ07506
34	32	3.6	1293	20	AAZ07506
35	32	3.6	1309	22	AAZ07506
36	32	3.6	1337	22	AAZ07506
37	32	3.6	1352	22	AAZ07506
38	32	3.6	1522	20	AAZ07506
39	32	3.6	1522	20	AAZ07506
40	32	3.6	1522	20	AAZ07506
41	32	3.6	1522	20	AAZ07506
42	32	3.6	1522	20	AAZ07506
43	32	3.6	1522	20	AAZ07506
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## ALIGNMENTS

RESULT 1	AAZ07516	standard; cDNA; 1708 BP.
ID	AAZ07516	
AC	AAZ07516	
XX		
DT	26-NOV-1999	(first entry)
XX		
DE	Rat HICP polypeptide encoding cDNA.	
XX		
KW	Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;	
KW	cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.	
OS	Rattus sp.	
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PN	W09947556-A2.	
XX		
PD	23-SEP-1999.	
XX		
PF	18-MAR-1999;	99WO-US05999.
XX		
PR	19-MAR-1998;	98US-0044273.
XX		
PA	(TUFTS ) TUFTS COLLEGE.	
XX		
PI	Castellot JJ;	
XX		
DR	WPI: 1999-562060/47.	
DR	P-PSDB: AAZ27434.	
XX		
PT	Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications	

XX Claim 2: Fig 1: 108bp: English.

CC This cDNA encodes a rat heparin-induced CCN-like protein (HICP) protein.  
 CC Agents that stimulate or inhibit HICP protein activity or expression,  
 CC antisense HICP nucleic acid molecules and HICP antibodies, can be used to  
 CC modulate cell-associated activity. HICP modulators can be used to treat  
 CC disorders characterized by aberrant HICP protein activity or expression.  
 CC Probes capable of hybridizing to HICP mRNA or antibodies specific for  
 CC HICP can be used to detect HICP activity in a biological sample. HICP  
 CC can be used to treat disorders, such as a cardiovascular or fibrotic  
 CC disorder, characterized by aberrant cell proliferation.

XX Sequence 1708 BP; 362 A; 486 C; 478 G; 382 T; 0 other;

Query Match 100.0%; Score 883; DB 20; Length 1708;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 883; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGCTTGTGATTCAGAGAGACCTGGGGTGGAGAGGGCCCTGGCAAGCTGAGCC 60  
 DB 1 GACGCTTGTGATTCAGAGAGACCTGGGGTGGAGAGGGCCCTGGCAAGCTGAGCC 60  
 QY 61 GCTGGGACAGTGGCTTGAATGAGAGCTTTATTACTGGGAAGCTAGAGAGCTC 120  
 DB 61 GCTGGGACAGTGGCTTGAATGAGAGCTTTATTACTGGGAAGCTAGAGAGCTC 120  
 QY 121 CTGTCAAGCTTGTCTTAAAGCTTAAAGCTTGTGGCTTGGGCTTCAACACTGTGAGA 180  
 DB 121 CTGTCAAGCTTGTCTTAAAGCTTAAAGCTTGTGGCTTGGGCTTCAACACTGTGAGA 180  
 QY 181 CACCTTGTGTGGTGGCTTCAAGGCTTCAAGCTTGTGGCTTGGGCTTCAAGGCTTCA 240  
 DB 181 CACCTTGTGTGGTGGCTTCAAGGCTTCAAGCTTGTGGCTTGGGCTTCAAGGCTTCA 240  
 QY 241 AGCGTACATGAGGGGACGCGCATGATCTTGTGGCACTTCTTCTTCTTCTTCTTCTT 300  
 DB 241 AGCGTACATGAGGGGACGCGCATGATCTTGTGGCACTTCTTCTTCTTCTTCTTCTTCTT 300  
 QY 301 TCTCAATGTGTGTGGGACGCTGCGGACACCTGTGCTTCTTCTTCTTCTTCTTCTTCTT 360  
 DB 301 TCTCAATGTGTGTGGGACGCTGCGGACACCTGTGCTTCTTCTTCTTCTTCTTCTTCTT 360  
 QY 361 AGTGGCCACAGGGGGTACCCCTGTGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 420  
 DB 361 AGTGGCCACAGGGGGTACCCCTGTGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 420  
 QY 421 GAGGGTGGGGAGTCTGTGACACCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGT 480  
 DB 421 GAGGGTGGGGAGTCTGTGACACCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGT 480  
 QY 481 GTGAGCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 DB 481 GTGAGCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 QY 541 GTAGCTGTGAGTGAATGGCCAGAGTACCTGATGATGATGATGATGATGATGATGATG 600  
 DB 541 GTAGCTGTGAGTGAATGGCCAGAGTACCTGATGATGATGATGATGATGATGATGATG 600  
 QY 601 GGGTCTGTGGGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 DB 601 GGGTCTGTGGGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 QY 661 TGGGGTGGCCAGCTGGGAGTGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
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 DB 721 GCGCCAGTGGGATGTGACACGAGGAGTACACGCGGATGACGCGCTCCACGCGGCAAG 780  
 QY 781 GACACCACTTTTGTGCTTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCT 840  
 DB 781 GACACCACTTTTGTGCTTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCT 840

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 QY 841 GCACAGCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 883  
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RESULT 2  
 AAZ07517  
 ID AAZ07517 standard; cDNA: 753 BP.

AC AAZ07517;

XX 26-NOV-1999 (first entry)

XX Rat HICP polypeptide coding sequence.

KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;  
 KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.

XX Rattus sp.

XX W09947556-A2.

XX 23-SEP-1999.

XX 18-MAR-1999; 99MO-US05999.

XX 19-MAR-1998; 98US-0044273.

XX (TUFT) TUFTS COLLEGE.

XX Castellot JJ;

XX WPI: 1999-562060/47.

XX P-PSDB; AAZ74434.

PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,  
 used in methods to identify modulators or in diagnostic applications

XX Claim 5: Fig 1: 108bp: English.

CC The invention provides a rat heparin-induced CCN-like protein (HICP)  
 CC protein. Agents that stimulate or inhibit HICP protein activity or  
 CC expression, antisense HICP nucleic acid molecules and HICP antibodies,  
 CC can be used to modulate cell-associated activity. HICP modulators can be  
 CC used to treat disorders characterized by aberrant HICP protein activity  
 CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies  
 CC specific for HICP can be used to detect HICP activity in a biological  
 CC sample. HICP can be used to treat disorders, such as a cardiovascular or  
 CC fibrotic disorder, characterized by aberrant cell proliferation. The  
 CC present sequence represents the coding sequence of rat HICP.

SO Sequence 753 BP; 132 A; 235 C; 230 G; 156 T; 0 other;

Query Match 71.9%; Score 635; DB 20; Length 753;

Best Local Similarity 100.0%; Pred. No. 1.4e-292; Mismatches 0; Indels 0; Gaps 0;

Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 ATGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 308  
 DB 1 ATGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60  
 QY 309 GTGTGTGGCCAGCTGTGGGAGACCCCTTACTGTGCTTGGACACACCCAGTGGCCA 368  
 DB 61 GTGTGTGGCCAGCTGTGGGAGACCCCTTACTGTGCTTGGACACACCCAGTGGCCA 120  
 QY 369 CAGGGGATACCCCTGTGTGATGTGCTGTGATGTGCTGTGATGTGCTGTGATGTGCTG 428  
 DB 121 CAGGGGATACCCCTGTGTGATGTGCTGTGATGTGCTGTGATGTGCTGTGATGTGCTG 180  
 QY 429 GGGGATCTGTGGACACCTGATGTGTGACACCCAGGAGGAGGAGGAGGAGGAGGAGGAG 488  
 DB 429 GGGGATCTGTGGACACCTGATGTGTGACACCCAGGAGGAGGAGGAGGAGGAGGAGGAG 488

Db 181 GGGGAGTCTCGACGACCCATGCTGACGACCCGACGAGGCTGTTGTACGCT 240  
Qy 489 GGGGAGGAGGCTGGGAGGATGGGAGTGTGTCTCTGTGATGAGATGAGGATGAGTGT 548  
Db 241 GGGGAGGAGGCTGGGAGGATGGGAGTGTGTCTCTGTGATGAGATGAGGATGAGTGT 300  
Qy 549 GAGGTGAATGGCCGAGGTACCTGATGAGAGACCTTTAAACCAATTGACAGGCTCTG 608  
Db 301 GAGGTGAATGGCCGAGGTACCTGATGAGAGACCTTTAAACCAATTGACAGGCTCTG 360  
Qy 609 TGCCGCTGTGATGAGAGTGTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668  
Db 361 TGCCGCTGTGATGAGAGTGTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Qy 669 CCCAGCTGGAGTGGCCGAGGAGGAGATGAGAGTGGAGGAGGAGGAGGAGGAGGAGGAG 728  
Db 421 CCCAGCTGGAGTGGCCGAGGAGGAGATGAGAGTGGAGGAGGAGGAGGAGGAGGAGGAG 480  
Qy 729 TGGGTATGTGACAGGAGTGTGACACCGGATCCAGGCTCCAGGCGGCAAGAGACCA 788  
Db 481 TGGGTATGTGACAGGAGTGTGACACCGGATCCAGGCTCCAGGCGGCAAGAGACCA 540  
Qy 789 CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848  
Db 541 CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Qy 849 TGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883  
Db 601 TGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635

RESULT 3  
AAZ07521

ID AAZ07521 standard; cDNA: 681 BP.

AAZ07521:

26-NOV-1999 (first entry)

Rat HICP mature polypeptide coding sequence.

Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.

Rattus sp.

W09947556-A2.

23-SEP-1999.

18-MAR-1999; 99WO-US05999.

19-MAR-1998; 98US-0044273.

(TUFT ) TUFTS COLLEGE.

Castellot JJ:

WPI: 1999-562060/47.

P-PSDB: AAY27440.

Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications.

Disclosure: Fig 2, 108pp; English.

The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological

CC sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The CC present sequence represents the coding sequence of rat HICP mature polypeptide.

SO Sequence 681 BP; 121 A; 211 C; 215 G; 134 T; 0 other;

Query Match 64.1%; Score 566; DB 20; Length 681;  
Best Local Similarity 100.0%; Pred. No. 1,1e-259;  
Matches 566; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 318 CAGCTGTGCGGAGACCCCTGACCTGTCTTGGACACACCCAGTGGCCAGGGGTA 377  
Db 1 CAGCTGTGCGGAGACCCCTGACCTGTCTTGGACACACCCAGTGGCCAGGGGTA 60  
Qy 378 CCCCTGTGTGATGT 437  
Db 61 CCCCTGTGTGATGT 120  
Qy 438 TGGACACCTGATGT 497  
Db 121 TGGACACCTGATGT 180  
Qy 498 CCTGCGGCGCATGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 557  
Db 181 CCTGCGGCGCATGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240  
Qy 558 GCGCGGAGTACCTGT 617  
Db 241 GCGCGGAGTACCTGT 300  
Qy 618 GATGACGCTGT 677  
Db 301 GATGACGCTGT 360  
Qy 678 GACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 737  
Db 361 GACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
Qy 738 GACCAAGGAGT 797  
Db 421 GACCAAGGAGT 480  
Qy 798 CTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 857  
Db 481 CTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Qy 858 TGCTCAACACCTGTGGGCTGGGAT 883  
Db 541 TGCTCAACACCTGTGGGCTGGGAT 566

RESULT 4  
AAZ07519

ID AAZ07519 standard; cDNA: 210 BP.

AAZ07519:

26-NOV-1999 (first entry)

Rat HICP IGFBP domain encoding cDNA.

Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder; insulin-like growth factor binding protein; IGFBP.

Rattus sp.

W09947556-A2.

23-SEP-1999.

18-MAR-1999; 99WO-US05999.

```

XX 19-MAR-1998; 98US-0044273.
XX (TUFT ) TUFTS COLLEGE.
XX Castellot JJ;
XX WPI; 1999-562060/47.
XX P-PSDB; AAY27438.
XX Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
XX used in methods to identify modulators or in diagnostic applications.
XX Disclosure; Page 104; 108bp; English.
XX PS
XX CC The invention provides a rat heparin-induced CCN-like protein (HICP)
XX CC protein. Agents that stimulate or inhibit HICP protein activity or
XX CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
XX CC can be used to modulate cell-associated activity. HICP modulators can be
XX CC used to treat disorders characterized by aberrant HICP protein activity
XX CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
XX CC specific for HICP can be used to detect HICP activity in a biological
XX CC sample. HICP can be used to treat disorders, such as a cardiovascular or
XX CC fibrotic disorder, characterized by aberrant cell proliferation. The
XX CC present sequence represents a nucleotide sequence encoding the insulin-
XX CC like growth factor binding protein (IGFBP) domain of HICP polypeptide.
XX SQ
XX Sequence 210 BP; 27 A; 65 C; 74 G; 44 T; 0 other;
XX
XX Query Match 23.8%; Score 210; DB 20; Length 210;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-90;
XX Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 318 CAGCTGTGGCGGACACCTGTACTCTCTTGGACACAGCCAGTGGCCACAGGGGTA 377
XX DB 1 CAGCTGTGGCGGACACCTGTACTCTCTTGGACACAGCCAGTGGCCACAGGGGTA 60
XX QY 378 CCCCTGTGCTGTGATGGCTGTGCTCTTAAAGTGTGGACGAGAGGCTGGGGAGTCC 437
XX DB 61 CCCCTGTGCTGTGATGGCTGTGCTCTTAAAGTGTGGACGAGAGGCTGGGGAGTCC 120
XX QY 438 TGGGACACCTGTGATGTGGACAGCCAGGAGGCTGTTGTAGCCTGGGGAGG 497
XX DB 121 TGGGACACCTGTGATGTGGACAGCCAGGAGGCTGTTGTAGCCTGGGGAGG 180
XX QY 498 CCTGGCGGCGCATGGGCTGTGTCTCTTG 527
XX DB 181 CCTGGCGGCGCATGGGCTGTGTCTCTTG 210
XX
XX RESULT 5
XX AA207518
XX ID AA207518 standard; cDNA; 177 BP.
XX AC AA207518;
XX AC 26-NOV-1999 (first entry)
XX DT
XX DE Rat HICP VWC domain encoding cDNA.
XX XX
XX KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss.
XX KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;
XX KW Von Willebrand C domain; VWC.
XX XX
XX OS Ratus sp.
XX PN MO9947556-A2.
XX PD 23-SEP-1999.
XX PF 18-MAR-1999; 99MO-US05999.
XX PR 19-MAR-1998; 98US-0044273.

```

```

XX (TUFT ) TUFTS COLLEGE.
XX Castellot JJ;
XX WPI; 1999-562060/47.
XX P-PSDB; AAY27436.
XX Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
XX used in methods to identify modulators or in diagnostic applications.
XX Disclosure; Page 103; 108bp; English.
XX PS
XX CC The invention provides a rat heparin-induced CCN-like protein (HICP)
XX CC protein. Agents that stimulate or inhibit HICP protein activity or
XX CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
XX CC can be used to modulate cell-associated activity. HICP modulators can be
XX CC used to treat disorders characterized by aberrant HICP protein activity
XX CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
XX CC specific for HICP can be used to detect HICP activity in a biological
XX CC sample. HICP can be used to treat disorders, such as a cardiovascular or
XX CC fibrotic disorder, characterized by aberrant cell proliferation. The
XX CC present sequence represents a cDNA encoding the Von Willebrand C (VWC)
XX CC a domain of the HICP polypeptide.
XX SQ
XX Sequence 177 BP; 35 A; 47 C; 60 G; 35 T; 0 other;
XX
XX Query Match 20.0%; Score 177; DB 20; Length 177;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-74;
XX Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 546 TGTGAGTGAATGCGCGGACGTAAGTGTGATGAGAGACTTTAAACCAATTCAGAGGTC 605
XX DB 1 TGTGAGTGAATGCGCGGACGTAAGTGTGATGAGAGACTTTAAACCAATTCAGAGGTC 60
XX QY 606 CTGTGCGGCTGTGATGAGAGGCTGTGCTTCACTGCTGCGCTGTCAGTGAATGAGG 665
XX DB 61 CTGTGCGGCTGTGATGAGAGGCTGTGCTTCACTGCTGCGCTGTCAGTGAATGAGG 120
XX QY 666 CTGCCAGCTGGGACTGCCACGCCCCAAGAGATACAGGTGCCAGAAAGTCTGC 722
XX DB 121 CTGCCAGCTGGGAGTGGAGTGGCCAGCCCAAGAGATACAGGTGCCAGAAAGTCTGC 177
XX
XX RESULT 6
XX AA276489/c
XX ID AA276489 standard; DNA; 753 BP.
XX AC AA276489;
XX AC 06-AUG-1999 (first entry)
XX DT
XX DE Mouse WISP-2 protein complementary nucleotide sequence SEQ ID NO:18.
XX XX
XX KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
XX KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
XX KW leukaemia; lymphoid malignancy; hematopoiesis-related disorder;
XX KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
XX KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
XX KW connective tissue disorder; catabolic state; inflammation;
XX KW testicular-related disorder; angiogenesis; immunological disorder; ss.
XX XX
XX OS Mus sp.
XX PN MO9921998-A1.
XX PD 06-MAY-1999.
XX PF 29-OCT-1998; 98MO-US22991.
XX PR 14-APR-1998; 98US-0081695.
XX PR 29-OCT-1997; 97US-0063704.
XX PR 03-FEB-1998; 98US-0073612.

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XX (GETH ) GENENTECH INC.  
PA Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;  
XX Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;  
PI WPI; 1999-337420/28.  
XX  
XX New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3  
PT Disclosure; Page 179-180; 284pp; English.  
XX  
XX The present invention describes Wnt-1 induced secreted polypeptides,  
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2  
CC and WISP-3 have homology to connective tissue growth factor (CTGF).  
CC Products from the present invention can be used to treat WISP-related  
CC disorders such as breast, ovarian, and colon cancer or melanoma. The  
CC products can be used to treat arteriosclerosis. The products can also be  
CC used to treat other diseases e.g. benign and malignant tumours,  
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,  
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and  
CC blastocoele disorders, hematopoiesis-related disorders, tissue-growth  
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney  
CC disorders, bone-related disorders such as osteoporosis, trauma such as  
CC burns, incisions, and other wounds, connective tissue disorders,  
CC catabolic states, testicular-related disorders, and inflammatory,  
CC angiogenic and immunologic disorders including arteriosclerosis. The  
CC products can also be used for detection and diagnosis especially of  
CC individuals with neoplastic cell growth or proliferation. The products  
CC can be used in the production of transgenic or knock-out animals.  
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing  
CC cells.  
XX  
SQ Sequence 753 BP; 159 A; 229 C; 238 G; 127 T; 0 other;  
Query Match 10.2%; Score 90; DB 20; Length 753;  
Best Local Similarity 100.0%; Pred. No. 7.8e-33;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 410 AGTGTGTCACGGAGGCTGGGGGAGTCTGCGACCACTGATGTCGACCCAGCCA 469  
DB 592 AGTGTGTCACGGAGGCTGGGGGAGTCTGCGACCACTGATGTCGACCCAGCCA 533  
QY 470 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 499  
DB 532 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 503  
RESULT 7  
AA76488  
ID AAX76488 standard; DNA; 1734 BP.  
XX  
AC AAX76488;  
XX  
XX 06-AUG-1999 (first entry)  
DE Mouse WISP-2 protein nucleotide sequence SEQ ID NO:17.  
XX  
XX WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;  
KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;  
KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;  
KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;  
KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;  
KW connective tissue disorder; catabolic state; inflammation;  
KW testicular-related disorder; angiogenesis; immunological disorder; ss.  
XX  
XX Mus sp.  
XX  
XX WO9921998-A1.  
XX  
XX 06-MAY-1999.  
XX  
XX 29-OCT-1998; 98WO-US22991.

XX 14-APR-1998; 98US-0081695.  
PR 29-OCT-1997; 97US-0063704.  
PR 03-FEB-1998; 98US-0073612.  
XX  
XX (GETH ) GENENTECH INC.  
PA Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;  
XX Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;  
PI WPI; 1999-337420/28.  
XX  
XX P-PSDB; AAX17651.  
DR  
XX  
XX New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3  
PT Example 2; Page 178-179; 284pp; English.  
XX  
XX The present invention describes Wnt-1 induced secreted polypeptides,  
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2  
CC and WISP-3 have homology to connective tissue growth factor (CTGF).  
CC Products from the present invention can be used to treat WISP-related  
CC disorders such as breast, ovarian, and colon cancer or melanoma. The  
CC products can be used to treat arteriosclerosis. The products can also be  
CC used to treat other diseases e.g. benign and malignant tumours,  
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,  
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and  
CC blastocoele disorders, hematopoiesis-related disorders, tissue-growth  
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney  
CC disorders, bone-related disorders such as osteoporosis, trauma such as  
CC burns, incisions, and other wounds, connective tissue disorders,  
CC catabolic states, testicular-related disorders, and inflammatory,  
CC angiogenic and immunologic disorders including arteriosclerosis. The  
CC products can also be used for detection and diagnosis especially of  
CC individuals with neoplastic cell growth or proliferation. The products  
CC can be used in the production of transgenic or knock-out animals.  
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing  
CC cells.  
XX  
SQ Sequence 1734 BP; 355 A; 491 C; 495 G; 393 T; 0 other;  
Query Match 10.2%; Score 90; DB 20; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 7.5e-33;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 410 AGTGTGTCACGGAGGCTGGGGGAGTCTGCGACCACTGATGTCGACCCAGCCA 469  
DB 418 AGTGTGTCACGGAGGCTGGGGGAGTCTGCGACCACTGATGTCGACCCAGCCA 477  
QY 470 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 499  
DB 478 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 507  
RESULT 8  
AA207520  
ID AA207520 standard; CDNA; 174 BP.  
XX  
AC AA207520;  
XX  
XX 26-NOV-1999 (first entry)  
DE Rat HICP TSPI domain encoding CDNA.  
XX  
XX Heparin-induced CN-1-like protein; HICP; cell-associated activity; ss;  
KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;  
KW thrombospondin I domain; TSPI.  
XX  
XX Rattus sp.  
XX  
XX WO9947556-A2.  
XX  
XX 23-SEP-1999.  
XX

PF 18-MAR-1999: 99WO-US05999.  
 PR 19-MAR-1998: 980S-0044273.  
 XX  
 PA (TUFT ) TUFTS COLLEGE.  
 XX  
 PI Castellot JJ;  
 XX  
 DR WPI; 1999-562060/47.  
 XX P-PDB; AAY27439.  
 XX  
 PT Nucleic acid sequences encoding rat heparin-induced CN-like protein.  
 PT used in methods to identify modulators or in diagnostic applications.  
 XX  
 PS Disclosure; Page 105; 108pp; English.  
 XX  
 CC The invention provides a rat heparin-induced CN-like protein (HICP)  
 CC protein. Agents that stimulate or inhibit HICP protein activity or  
 CC expression, antisense HICP nucleic acid molecules and HICP antibodies,  
 CC can be used to modulate cell-associated activity. HICP modulators can be  
 CC used to treat disorders characterized by aberrant HICP protein activity  
 CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies  
 CC specific for HICP can be used to detect HICP activity in a biological  
 CC sample. HICP can be used to treat disorders, such as a cardiovascular or  
 CC fibrotic disorder, characterized by aberrant cell proliferation. The  
 CC present sequence represents a nucleotide sequence encoding the  
 CC thrombospondin 1 (TSP1) domain of the HICP polypeptide.  
 CC  
 SQ Sequence 174 BP; 36 A; 62 C; 45 G; 31 T; 0 other;  
 XX  
 Query Match 6.7%; Score 59; DB 20; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-18;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 825 CCTGTCCAAATTGGACAGACAGCTGGGCCCCCTGCTCAACCACTGTGGCGTGGGCAT 883  
 DB 1 CCTGTCCAAATTGGACAGACAGCTGGGCCCCCTGCTCAACCACTGTGGCGTGGGCAT 59  
 XX  
 RESULT 9  
 ID ABA72245  
 XX ABA72245 standard; DNA; 199 BP.  
 AC ABA72245;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX  
 DE Human foetal liver single exon nucleic acid probe #20550.  
 XX  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157277-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-483447/52.  
 XX

PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human fetal liver -  
 XX  
 PS Claim 4; SEQ ID NO 20550; 639pp + sequence listing; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a single exon nucleic acid  
 CC probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;  
 XX  
 Query Match 3.6%; Score 32; DB 22; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 654 GAGGATGTCGGCTGCCAGCTGGAGCTGCC 685  
 DB 129 GAGGATGTCGGCTGCCAGCTGGAGCTGCC 160  
 XX  
 RESULT 10  
 ID ABA38112  
 XX ABA38112 standard; DNA; 199 BP.  
 AC ABA38112;  
 XX  
 DT 23-JAN-2002 (first entry)  
 XX  
 DE Probe #16578 for gene expression analysis in human heart cell sample.  
 XX  
 KW Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157274-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00666.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488899/53.  
 XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts -  
 XX  
 PS Claim 4; SEQ ID NO 16578; 530pp; English.  
 XX  
 CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart. The  
 CC present sequence is one such probe. The probes may be used for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from the human heart via microarrays. By measuring gene expression, the  
 CC probes are useful for predicting, diagnosing, grading, staging,

CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX

Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match 3.6%; Score 32; DB 22; Length 199;  
Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GAGGATGTCGCGCTGCCAGCTGGGACTGCC 685  
Db 129 GAGGATGTCGCGCTGCCAGCTGGGACTGCC 160

RESULT 11  
AAK20667  
ID AAK20667 standard; DNA; 199 BP.  
XX  
AC AAK20667;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe SEQ ID NO: 20658.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe;  
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
KW epilepsy; cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00667.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0633366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483446/52.  
XX

Single exon nucleic acid probes for analyzing gene expression in human  
PT brains -  
XX  
PS Example 4; SEQ ID NO: 20658; 650pp + Sequence Listing; English.  
XX

CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention.  
CC  
XX

Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match 3.6%; Score 32; DB 22; Length 199;  
Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GAGGATGTCGCGCTGCCAGCTGGGACTGCC 685  
Db 129 GAGGATGTCGCGCTGCCAGCTGGGACTGCC 160

RESULT 12  
AAK46811  
ID AAK46811 standard; DNA; 199 BP.  
XX  
AC AAK46811;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed single exon probe SEQ ID NO: 21368.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00668.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0633366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488900/53.  
XX

Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human bone marrow -  
XX  
PS Example 4; SEQ ID NO: 21368; 658pp + Sequence Listing; English.  
XX

CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
CC the probes of the invention.  
CC  
XX

Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match 3.6%; Score 32; DB 22; Length 199;  
Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GAGGATGTCGCGCTGCCAGCTGGGACTGCC 685  
Db 129 GAGGATGTCGCGCTGCCAGCTGGGACTGCC 160

RESULT 13  
AAI25749  
ID AAI25749 standard; DNA; 199 BP.  
XX  
AC AAI25749;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Probe #15682 for gene expression analysis in human cervical cell sample.  
XX







GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:50:06 ; Search time 48.2525 Seconds  
(without alignments)  
5612.050 Million cell updates/sec

Title: US-10-010-408-1\_COPY\_1\_883  
Perfect score: 883  
Sequence: 1 GAGCGCTTCGATCTCCAGAG.....ACCACCTGTGGCTGGCGCAT 883

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCtUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	90	10.2	1734 4	US-09-182-145-17 Sequence 17, Appl
2	90	10.2	1734 4	US-09-182-145-18 Sequence 18, Appl
3	32	3.6	738 4	US-09-182-145-38 Sequence 38, Appl
4	32	3.6	841 4	US-09-182-145-39 Sequence 39, Appl
5	32	3.6	1293 4	US-09-182-145-13 Sequence 13, Appl
6	32	3.6	1293 4	US-09-182-145-14 Sequence 14, Appl
7	27	3.1	51 4	US-09-182-145-117 Sequence 117, App
8	19	2.2	616 4	US-09-385-982-220 Sequence 220, App
9	19	2.2	1196 4	US-09-149-476-225 Sequence 225, App
10	19	2.2	1220 4	US-09-149-476-57 Sequence 57, Appl
11	19	2.2	1514 2	US-09-213-768-1 Sequence 1, Appl
12	19	2.2	1539 4	US-09-668-680-13 Sequence 13, Appl
13	18	2.0	20 2	US-09-213-768-2 Sequence 2, Appl
14	18	2.0	2949 4	US-08-259-451-10 Sequence 10, Appl
15	18	2.0	3727 1	US-08-249-380-1 Sequence 1, Appl
16	18	2.0	8957 4	US-08-259-451-1 Sequence 1, Appl
17	17	1.9	44 4	US-09-182-145-152 Sequence 152, App
18	17	1.9	480 3	US-09-188-930-206 Sequence 206, App
19	17	1.9	614 4	US-08-998-416-151 Sequence 151, App
20	17	1.9	661 4	US-08-578-634C-3 Sequence 3, Appl
21	17	1.9	661 4	US-09-430-010-3 Sequence 3, Appl
22	17	1.9	896 3	US-09-188-930-36 Sequence 36, Appl
23	17	1.9	933 3	US-08-987-743-5 Sequence 5, Appl
24	17	1.9	1308 3	US-08-987-743-5 Sequence 5, Appl
25	17	1.9	1491 4	US-09-662-249A-3 Sequence 3, Appl
26	17	1.9	1743 3	US-08-665-259-20 Sequence 20, Appl
27	17	1.9	1743 3	US-08-762-500-20 Sequence 20, Appl

28	17	1.9	1821 4	US-09-149-476-90 Sequence 90, Appl
29	17	1.9	1974 3	US-08-762-500-78 Sequence 78, Appl
30	17	1.9	2517 3	US-08-733-360A-4 Sequence 4, Appl
31	17	1.9	2517 3	US-08-987-743-16 Sequence 16, Appl
32	17	1.9	3217 4	US-08-916-935-4 Sequence 4, Appl
33	17	1.9	3280 4	US-09-484-970B-43 Sequence 43, Appl
34	17	1.9	3865 4	US-09-149-476-296 Sequence 296, App
35	17	1.9	6803 3	US-08-665-259-19 Sequence 19, Appl
36	17	1.9	6803 3	US-08-762-500-19 Sequence 19, Appl
37	17	1.9	7874 4	US-09-780-175-95 Sequence 95, Appl
38	17	1.9	35828 4	US-09-449-218D-17 Sequence 17, Appl
39	17	1.9	81001 4	US-09-750-580-1 Sequence 1, Appl
40	17	1.9	111282 4	US-09-754-250-3 Sequence 3, Appl
41	16	1.8	31 1	US-08-524-757-34 Sequence 34, Appl
42	16	1.8	428 4	US-09-397-787-224 Sequence 224, App
43	16	1.8	435 4	US-09-397-787-280 Sequence 280, App
44	16	1.8	540 2	US-08-726-306A-182 Sequence 182, App
45	16	1.8	572 4	US-09-342-653-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-09-182-145-17  
Sequence 17, Application US/09182145B  
Patent No. 6387657  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WSP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P117672  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 17  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-182-145-17  
Query Match 10.2% Score 90; DB 4; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 2.7e-34;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 410 AGTGTGTCACGAGGAGCTGGGAGTCTGCGACACCTGATGTCGAGCCAGCA 469  
418 AGTGTGTCACGAGGAGCTGGGAGTCTGCGACACCTGATGTCGAGCCAGCA 477  
QY 470 GGGCTGTTGTGACCTGGGCGAGGCC 499  
DB 478 GGGCTGTTGTGACCTGGGCGAGGCC 507  
RESULT 2  
US-09-182-145-18/C  
Sequence 18, Application US/09182145B  
Patent No. 6387657  
GENERAL INFORMATION:

APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 18  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-182-145-18

Query Match 10.2%; Score 90; DB 4; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 2,7e-34;  
Matches: 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 ACTGTGTGCAGGAGGCTGGGAGTCTGCACACCACTGATGTCTGCCACCCAGCCA 469  
DB 1317 ACTGTGTGCAGGAGGCTGGGAGTCTGCACACCACTGATGTCTGCCACCCAGCCA 1258

QY 470 GGGCGCTGTTTGTGACGCTGGGGCAGGCC 499  
DB 1257 GGGCGCTGTTTGTGACGCTGGGGCAGGCC 1228

## RESULT 3

US-09-182-145-38  
Sequence 38, Application US/09182145B  
Patent No. 6387657

GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 38  
LENGTH: 738  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-182-145-38

Query Match 3.6%; Score 32; DB 4; Length 738;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches: 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 375 GTACCCCTGGTGTGATGGCTGGGCTGCTG 406  
DB 115 GTACCCCTGGTGTGATGGCTGGGCTGCTG 146

## RESULT 4

US-09-182-145-39  
Sequence 39, Application US/09182145B  
Patent No. 6387657

GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 39  
LENGTH: 841  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 1-841  
OTHER INFORMATION: Sequence is synthesized.  
Patent No. 6387657  
US-09-182-145-39

Query Match 3.6%; Score 32; DB 4; Length 841;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches: 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GAGATGTGCGGCTGCCAGCTGGGACTGCC 685  
DB 417 GAGATGTGCGGCTGCCAGCTGGGACTGCC 448

## RESULT 5

US-09-182-145-13  
Sequence 13, Application US/09182145B  
Patent No. 6387657

GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29



EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 13  
LENGTH: 1293  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-182-145-13

Query Match 3.6%; Score 32; DB 4; Length 1293;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGCTGCTG 406  
DB 148 GTACCCCTGCTGCTGATGGCTGCTGCTG 179

## RESULT 6

US-09-182-145-14/c  
Sequence 14, Application US/09182145B  
Patent No. 6387657  
GENERAL INFORMATION:

APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 14  
LENGTH: 1293  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-182-145-14

Query Match 3.6%; Score 32; DB 4; Length 1293;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGCTGCTG 406  
DB 146 GTACCCCTGCTGCTGATGGCTGCTGCTG 1115

## RESULT 7

US-09-182-145-117  
Sequence 117, Application US/09182145B  
Patent No. 6387657  
GENERAL INFORMATION:

APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.

APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 117  
LENGTH: 51  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1-51  
OTHER INFORMATION: Sequence is synthesized.  
US-09-182-145-117

Query Match 3.1%; Score 27; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.00081;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 CCTGCTGCTGATGGCTGCTGCTG 406  
DB 1 CCTGCTGCTGATGGCTGCTGCTG 27

## RESULT 8

US-09-385-982-220/c  
Sequence 220, Application US/09385982  
Patent No. 6262334  
GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.  
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
FILE REFERENCE: CCDNA-260XX  
CURRENT APPLICATION NUMBER: US/09/385,982  
EARLIER FILING DATE: 1999-08-30  
EARLIER APPLICATION NUMBER: 09/328,111  
EARLIER FILING DATE: 1999-06-08  
EARLIER APPLICATION NUMBER: 60/117,393  
EARLIER FILING DATE: 1999-01-27  
EARLIER APPLICATION NUMBER: 60/098,639  
EARLIER FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 544  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 220  
LENGTH: 616  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(616)  
OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-220

Query Match 2.2%; Score 19; DB 4; Length 616;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TGATGACGTGGCTTCACC 635  
DB 127 TGATGACGTGGCTTCACC 109

RESULT 9  
US-09-149-476-225/C  
Sequence 225, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
EARLIER APPLICATION NUMBER: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
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EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
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EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 2.2%; Score 19; DB 4; Length 1196;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 617 TGATGCGGTGCTCACC 635  
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DB 134 TGATGCGGTGCTCACC 116

RESULT 10  
US-09-149-476-57/c  
Sequence 57, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002p1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-06-06  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
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EARLIER APPLICATION NUMBER: 60/047,501  
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EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056,862  
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EARLIER APPLICATION NUMBER: 60/056,887  
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EARLIER APPLICATION NUMBER: 60/048,964  
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EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 2.2%; Score 19; DB 4; Length 1220;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TGATGACGTGCTTCACC 635  
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Db 128 TGATGACGTGCTTCACC 110

RESULT 11  
US-09-213-768-1/c  
; Sequence 1, Application US/09213768  
; Patent No. 5985664  
; GENERAL INFORMATION:  
; APPLICANT: Brenda F. Baker  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRYIN EXPRESSION  
; FILE REFERENCE: RTS-0026  
; CURRENT APPLICATION NUMBER: US/09/213,768  
; CURRENT FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1

LENGTH: 1514  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (136)..(441)  
US-09-213-768-1

Query Match 2.2%; Score 19; DB 2; Length 1514;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TGATGACGGTGGCTTCAC 635  
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DB 136 TGATGACGGTGGCTTCAC 118

RESULT 12  
US-09-668-680-13  
Sequence 13, Application US/09668680  
Patent No. 6436703  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Zhou, Ping  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aildong J.  
APPLICANT: Xu, Chongjun  
TITLE OF INVENTION: No. 6436703el Nucleic Acids and  
FILE REFERENCE: 790CIP2A  
CURRENT APPLICATION NUMBER: US/09/668, 680  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PL\_FL\_genes Version 2.0  
SEQ ID NO 13  
LENGTH: 1539  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (130)..(1539)  
US-09-668-680-13

Query Match 2.2%; Score 19; DB 4; Length 1539;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 CTTCCTGCTCTCTCA 305  
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DB 774 CTTCCTGCTCTCTCA 792

RESULT 13  
US-09-213-768-2/c  
Sequence 2, Application US/09213768  
Patent No. 5985664  
GENERAL INFORMATION:  
APPLICANT: Brenda F. Baker  
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION  
FILE REFERENCE: RFS-0026  
CURRENT APPLICATION NUMBER: US/09/213,768  
CURRENT FILING DATE: 1998-12-17  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 2

LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR Primer  
US-09-213-768-2

Query Match 2.0%; Score 18; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TGATGACGGTGGCTTCAC 634  
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DB 18 TGATGACGGTGGCTTCAC 1

RESULT 14  
US-08-259-451-10  
Sequence 10, Application US/08259451  
Patent No. 6406841  
GENERAL INFORMATION:  
APPLICANT: Lee, Helen H.  
APPLICANT: Swanson, Priscilla A.  
APPLICANT: Idler, Kenneth B.  
APPLICANT: Rosenblatt, Joseph D.  
APPLICANT: Chen, Irvin S. Y.  
APPLICANT: Golde, David W.  
APPLICANT: Robertson, Eugene F.  
APPLICANT: Stephens, John E.  
APPLICANT: Chan, Emerson W.  
APPLICANT: Buytendorp, Mark H.  
APPLICANT: Johnson, Joan E.  
APPLICANT: Motley, Cheryl T.  
APPLICANT: Peterson, Bryan  
APPLICANT: Edwards, Michelle  
APPLICANT: Guidinger, Peggy  
TITLE OF INVENTION: HTLV-II/III Compositions  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: One Abbott Park Road  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
MEDIUM TYPE: storage  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,451  
FILING DATE: 20-JUN-1994  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/086,415  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Daniel W. Collins  
REGISTRATION NUMBER: 31,912  
REFERENCE/DOCKET NUMBER: 5381 US.PI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 937-6365  
TELEFAX: (708) 938-2623  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2949 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear

US-08-259-451-10

Query Match 2.0%; Score 18; DB 4; Length 2949;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 GGCCTCCACGGCCTCACC 210  
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DB 2071 GGCCTCCACGGCCTCACC 2088

## RESULT 15

US-08-249-380-1/c  
; Sequence 1, Application US/08249380  
; Patent No. 5827685  
; GENERAL INFORMATION:  
; APPLICANT: Lindquist, Susan  
; TITLE OF INVENTION: Methods and Compositions of Genetic  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/249,380  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/710,187  
; FILING DATE: 31-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: ARCD:024  
; TELEPHONE: 713-787-1400  
; TELEFAX: 713-789-2679  
; INFORMATION FOR SEQ. ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3727 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-249-380-1

Query Match 2.0%; Score 18; DB 1; Length 3727;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 ACTGATCCATCTTCTGCC 280  
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DB 1143 ACTGATCCATCTTCTGCC 1126

Search completed: July 28, 2003, 15:58:53  
Job time : 49.2525 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model.

Run on: July 28, 2003, 14:30:21 ; Search time 217.455 Seconds  
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8377.033 Million cell updates/sec

Title: US-10-010-408-1\_COPY\_1\_883  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1439767 seqs, 1031500376 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	883	100.0	1708	US-10-010-408-1	Sequence 1, App11
2	635	71.9	753	US-10-010-408-3	Sequence 3, App11
3	566	64.1	681	US-10-010-408-12	Sequence 12, App1
4	210	23.8	210	US-10-010-408-8	Sequence 8, App1
5	177	20.0	177	US-10-010-408-5	Sequence 5, App1
6	90	10.2	1734	US-10-112-267-17	Sequence 17, App1
7	90	10.2	1734	US-10-112-267-18	Sequence 18, App1
8	59	6.7	174	US-10-010-408-10	Sequence 10, App1
9	32	3.6	199	US-09-864-761-23432	Sequence 23432, A
10	32	3.6	586	US-09-864-761-6698	Sequence 6698, Ap
11	32	3.6	738	US-10-112-267-38	Sequence 38, App1
12	32	3.6	841	US-10-112-267-39	Sequence 39, App1
13	32	3.6	1266	US-10-137-866-319	Sequence 319, App
14	32	3.6	1266	US-10-146-726-319	Sequence 319, App
15	32	3.6	1266	US-10-146-727-319	Sequence 319, App
16	32	3.6	1266	US-10-146-788-319	Sequence 319, App

17	32	3.6	1266	14	US-10-152-380-319	Sequence 319, App
18	32	3.6	1266	14	US-10-153-934-319	Sequence 319, App
19	32	3.6	1266	15	US-10-028-072-319	Sequence 319, App
20	32	3.6	1266	15	US-10-121-049-319	Sequence 319, App
21	32	3.6	1266	15	US-10-123-904-319	Sequence 319, App
22	32	3.6	1266	15	US-10-140-470-319	Sequence 319, App
23	32	3.6	1266	15	US-10-175-746-319	Sequence 319, App
24	32	3.6	1266	15	US-10-176-918-319	Sequence 319, App
25	32	3.6	1266	15	US-10-176-921-319	Sequence 319, App
26	32	3.6	1266	15	US-10-137-865-319	Sequence 319, App
27	32	3.6	1266	15	US-10-140-474-319	Sequence 319, App
28	32	3.6	1266	15	US-10-142-431-319	Sequence 319, App
29	32	3.6	1266	15	US-10-143-114-319	Sequence 319, App
30	32	3.6	1266	15	US-10-140-002-319	Sequence 319, App
31	32	3.6	1266	15	US-10-142-419-319	Sequence 319, App
32	32	3.6	1266	15	US-10-123-262-319	Sequence 319, App
33	32	3.6	1266	15	US-10-142-423-319	Sequence 319, App
34	32	3.6	1266	15	US-10-121-050-319	Sequence 319, App
35	32	3.6	1266	15	US-10-141-755-319	Sequence 319, App
36	32	3.6	1266	15	US-10-143-032-319	Sequence 319, App
37	32	3.6	1266	15	US-10-123-108-319	Sequence 319, App
38	32	3.6	1266	15	US-10-123-236-319	Sequence 319, App
39	32	3.6	1266	15	US-10-123-261-319	Sequence 319, App
40	32	3.6	1266	15	US-10-140-921-319	Sequence 319, App
41	32	3.6	1266	15	US-10-140-928-319	Sequence 319, App
42	32	3.6	1266	15	US-10-121-045-319	Sequence 319, App
43	32	3.6	1266	15	US-10-123-292-319	Sequence 319, App
44	32	3.6	1266	15	US-10-123-903-319	Sequence 319, App
45	32	3.6	1266	15	US-10-124-819-319	Sequence 319, App

ALIGNMENTS

RESULT 1  
US-10-010-408-1  
Sequence 1, Application US/10010408  
Publication No. US20020165185A1

GENERAL INFORMATION:  
APPLICANT: John J. Castelli et al.  
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCR-Like Molecules and Uses Therefor

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1708 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdna  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 249..1001  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-10-010-408-1

Query Match 100.0%; Score 883; DB 15; Length 1708;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 883; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGCTTGTATCTCAGAGAGACCCCTGGGGTGGACAGAGGACCTTGGCAAGGCTGAGGC 60  
 DB 1 GACGCTTGTATCTCAGAGAGACCCCTGGGGTGGACAGAGGACCTTGGCAAGGCTGAGGC 60  
 QY 61 GCTGGGCACTGGCTTGAATGAGGTCTTATTACTGGAACTGAGAGACTGAGAGCTC 120  
 DB 61 GCTGGGCACTGGCTTGAATGAGGTCTTATTACTGGAACTGAGAGACTGAGAGCTC 120  
 QY 121 CTGTACGCTTGTCTTAAATCTTACGACTTGTGTGGCTTGGCTTCAACACTGTGACA 180  
 DB 121 CTGTACGCTTGTCTTAAATCTTACGACTTGTGTGGCTTGGCTTCAACACTGTGACA 180  
 QY 181 CACCTTGTGTGGCTTCCACAGGCTCAGCTTCAAGCTTGAAGCTGGCTCCACAGAGGAC 240  
 DB 181 CACCTTGTGTGGCTTCCACAGGCTCAGCTTCAAGCTTGAAGCTGGCTCCACAGAGGAC 240  
 QY 241 ACGGTACATGAGAGGAGACCCACATGATCTTGTGGCCACTTCTCTCTGCTTC 300  
 DB 241 ACGGTACATGAGAGGAGACCCACATGATCTTGTGGCCACTTCTCTCTGCTTC 300  
 QY 301 TCTCAATGATGTGTGCCAGCTGTGGCGGACACCCGTACCTGCTTGGAGACCAACCC 360  
 DB 301 TCTCAATGATGTGTGCCAGCTGTGGCGGACACCCGTACCTGCTTGGAGACCAACCC 360  
 QY 361 AGTGGCCACAGGGGGTATCCCTGTGTGCTGATGAGTGGCTGTAAGTGTGACAC 420  
 DB 361 AGTGGCCACAGGGGGTATCCCTGTGTGCTGATGAGTGGCTGTAAGTGTGACAC 420  
 QY 421 GGAAGCTGGGGAGTCTCTGACACACCTCATGTCTGCAACCCACAGGGCTGTT 480  
 DB 421 GGAAGCTGGGGAGTCTCTGACACACCTCATGTCTGCAACCCACAGGGCTGTT 480  
 QY 481 GTACGCTGGGGAGGCTTGGGGGACATGGGGGCTGTGTCTTGGAGTGAAGATGAG 540  
 DB 481 GTACGCTGGGGAGGCTTGGGGGACATGGGGGCTGTGTCTTGGAGTGAAGATGAG 540  
 QY 541 GTAGCTGTGAGTGAATGAGCCAGAGTACCTGATGAGAGACCTTAAACCAATTGCA 600  
 DB 541 GTAGCTGTGAGTGAATGAGCCAGAGTACCTGATGAGAGACCTTAAACCAATTGCA 600  
 QY 601 GGGTCTGTGGCGCTGTATGACGGTGGCTTCACTGCTCCGCGCTGTCACTGAGTAG 660  
 DB 601 GGGTCTGTGGCGCTGTATGACGGTGGCTTCACTGCTCCGCGCTGTCACTGAGTAG 660  
 QY 661 TGGGGTGGCGAGCTGGGGAGTGGCCCAAGGATATACAGTGGCCAGAGAAATGCT 720  
 DB 661 TGGGGTGGCGAGCTGGGGAGTGGCCCAAGGATATACAGTGGCCAGAGAAATGCT 720  
 QY 721 GCCCGAGTGGGTATGTACAGAGAGTACACCGGCGATCCAGGCTCCACAGGCGCAG 780  
 DB 721 GCCCGAGTGGGTATGTACAGAGAGTACACCGGCGATCCAGGCTCCACAGGCGCAG 780  
 QY 781 GACACCACTTCTGCGCTTGTACTCTGTCTGTGTGATGCTCTCTTGTCCAAATTGGA 840  
 DB 781 GACACCACTTCTGCGCTTGTACTCTGTCTGTGTGATGCTCTCTTGTCCAAATTGGA 840  
 QY 841 GGACAGCTGGGGGCGCTGCTCAACCACTGTGGGTGGCAT 883  
 DB 841 GGACAGCTGGGGGCGCTGCTCAACCACTGTGGGTGGCAT 883

DB 841 GCACAGCTGGGGGCGCTGCTCAACCACTGTGGGTGGCAT 883

RESULT 2  
 US-10-010-408-3  
 Sequence 3, Application US/10010408  
 Publication No. US20020165185A1  
 GENERAL INFORMATION:  
 APPLICANT: John J. Castelli, Jr.  
 TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCR-Like Molecules  
 and Uses Therefor

NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/010,408  
 FILING DATE: 07-Dec-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/044,273  
 FILING DATE: March 19, 1998  
 APPLICATION NUMBER: <Unknown>

ATTORNEY/AGENT INFORMATION:  
 NAME: Amy E. Mandragouras  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: MB1-004

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)742-4214  
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 753 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdna  
 FEATURE:

NAME/KEY: CDS  
 LOCATION: 1..750  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-010-408-3

Query Match 71.9%; Score 635; DB 15; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 ATGAGGGAGGAGCCATGATTCATCTTGGGCACTTCTGCTGCTGCTTCAATG 308  
 DB 1 ATGAGGGAGGAGCCATGATTCATCTTGGGCACTTCTGCTGCTGCTTCAATG 60  
 QY 309 GTGTGTGCCAGCTGTGCCGAGACCCCTGTACTGTCTTGGACACACCCAGTGGCCA 368  
 DB 61 GTGTGTGCCAGCTGTGCCGAGACCCCTGTACTGTCTTGGACACACCCAGTGGCCA 120  
 QY 369 CAGGGGATACCCCTGTGTGATGGCTGTGCTGTGTAAGTGTGTGACAGAGGCTG 428  
 DB 121 CAGGGGATACCCCTGTGTGATGGCTGTGCTGTGTAAGTGTGTGACAGAGGCTG 180  
 QY 429 GGGAGTCCCTGGACACCTGATGTGCGACACCCAGAGGCTGGTTGTAGGCT 488  
 DB 181 GGGAGTCCCTGGACACCTGATGTGCGACACCCAGAGGCTGGTTGTAGGCT 240



489 GGGGAGGACCTTGGGCGCATGAGGGCTGTGTCTCTTGGATGAGGATGACGTAAGTCT 548  
241 GGGGAGGACCTTGGGCGCATGAGGGCTGTGTCTCTTGGATGAGGATGACGTAAGTCT 300  
549 GAGGTGATGAGGCGGAGGATGAGTGGAGAGACCTTTAAACCAATTGACGGTCTG 608  
301 GAGGTGATGAGGCGGAGGATGAGTGGAGAGACCTTTAAACCAATTGACGGTCTG 360  
609 TGCCGCTGTGATGAGGAGTGGCTTCACTGCTGCGCTGTGAGAGGATGAGGAGTGG 668  
361 TGCCGCTGTGATGAGGAGTGGCTTCACTGCTGCGCTGTGAGAGGATGAGGAGTGG 420  
669 CCCAGCTGGAGTGGCCAGGCCCCAAGAAATACAGTGCAGGAAAGTGTCTGCCCGAG 728  
421 CCCAGCTGGAGTGGCCAGGCCCCAAGAAATACAGTGCAGGAAAGTGTCTGCCCGAG 480  
729 TGGGTATGTGACACAGGAGTGCACACCGGATCCAGCGCTCCAGGCGGCAAGACCAA 788  
481 TGGGTATGTGACACAGGAGTGCACACCGGATCCAGCGCTCCAGGCGGCAAGACCAA 540  
789 CTTTGTGCTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848  
541 CTTTGTGCTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
849 TGGGCGCCCTGCTCAACCACTGTGGGCTGGGCAAT 883  
601 TGGGCGCCCTGCTCAACCACTGTGGGCTGGGCAAT 635

## RESULT 3

US-10-010-408-12  
Sequence 12, Application US/10010408  
Publication No. US20020165185A1

## GENERAL INFORMATION:

APPLICANT: John J. Castellot, Jr.  
TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules  
and Uses Therefor

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408

FILING DATE: 07-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/044,273

FILING DATE: March 19, 1998

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MBI-004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 681 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..681  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-010-408-12

Query Match  
Best Local Similarity 100.0%, Score 566; DB 15; Length 681;  
Matches 566; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

318 CAGCTGTGCGGAGACACCTGTACCTGTCTTGGACACACCCAGTCCACAGGGGTA 377  
1 CAGCTGTGCGGAGACACCTGTACCTGTCTTGGACACACCCAGTCCACAGGGGTA 60  
378 CCCCTGTGCTGAGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 437  
61 CCCCTGTGCTGAGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 120  
438 TCGACACACCTGATGTGTGCGACCCAGCCAGGCGCTGTGCTGTGCTGTGCTGTGCT 497  
121 TCGACACACCTGATGTGTGCGACCCAGCCAGGCGCTGTGCTGTGCTGTGCTGTGCT 180  
498 CCTGCGGCGCATGGGCTGTGTGTCTTGTGATGAGATGACGTAAGTGTGATGAT 557  
181 CCTGCGGCGCATGGGCTGTGTGTCTTGTGATGAGATGACGTAAGTGTGATGAT 240  
558 GGGCGGAGTACCTGATGAGAGACCTTTAAACCAATGAGGCTCTGTGCGGCTGT 617  
241 GGGCGGAGTACCTGATGAGAGACCTTTAAACCAATGAGGCTCTGTGCGGCTGT 300  
618 GATGAGGTGTGCTGACCTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677  
301 GATGAGGTGTGCTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
678 GACTGCCACACGCCCCAAGAGATACAGTGTCCAGAAAGTGTGCTGCCAGTGTGT 737  
361 GACTGCCACACGCCCCAAGAGATACAGTGTCCAGAAAGTGTGCTGCCAGTGTGT 420  
738 GACGAGGAGTGTGACACCGGCGATCCAGGCGTCCAGGCGCAAGACCAATTTCTGCC 797  
421 GACGAGGAGTGTGACACCGGCGATCCAGGCGTCCAGGCGCAAGACCAATTTCTGCC 480  
798 CTTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 857  
481 CTTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
858 TGTCTAACCACTGTGGGCTGGGCAAT 883  
541 TGTCTAACCACTGTGGGCTGGGCAAT 566

## RESULT 4

US-10-010-408-8  
Sequence 8, Application US/10010408  
Publication No. US20020165185A1

## GENERAL INFORMATION:

APPLICANT: John J. Castellot, Jr.  
TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules  
and Uses Therefor

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..210  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-010-408-8

Query Match 23.8%; Score 210; DB 15; Length 210;  
Best Local Similarity 100.0%; Pred. No. 3.9e-99;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 318 CACCTGTGCGGACACCTGTACCTGTCTTGACACACCCACAGTGCACAGGGGTA 377  
DB 1 CACCTGTGCGGACACCTGTACCTGTCTTGACACACCCACAGTGCACAGGGGTA 60  
QY 378 CCCCTGTGTGATGGCTGTGGCTGTCTGTAAGTGTGTGCACAGAGGCTGGGGAGTCC 437  
DB 61 CCCCTGTGTGATGGCTGTGGCTGTCTGTAAGTGTGTGCACAGAGGCTGGGGAGTCC 120  
QY 438 TGGGACACCTGATGTGTGCAGACCCAGCCAGGAGGCTGTGTGTCAGCTGGGGAGGC 497  
DB 121 TGGGACACCTGATGTGTGCAGACCCAGCCAGGAGGCTGTGTGTCAGCTGGGGAGGC 180  
QY 498 CCTGGGCGCCATGGGGCTGTGTCTCTTG 527  
DB 181 CCTGGGCGCCATGGGGCTGTGTCTCTTG 210

RESULT 5  
US-10-010-408-5  
Sequence 5, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castelfr. Jr.  
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..177  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-010-408-5

Query Match 20.0%; Score 177; DB 15; Length 177;  
Best Local Similarity 100.0%; Pred. No. 6.1e-82;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 546 TGTGAGGTGAGTGGCCGACAGTACCTGATGAGAGACCTTTAAACCAATTGCAGGGTC 605  
DB 1 TGTGAGGTGAGTGGCCGACAGTACCTGATGAGAGACCTTTAAACCAATTGCAGGGTC 60  
QY 606 CTGTGGCGGTGATGACGTGTGCTTACCTGCTGCCCTGTGCAGTGAATGTCGGG 665  
DB 61 CTGTGGCGGTGATGACGTGTGCTTACCTGCTGCCCTGTGCAGTGAATGTCGGG 120  
QY 666 CTGCCAGCTGTGAGTGTGCCACGCCCAAGAGATACAGGTGCCAGAAAGTCTGC 722  
DB 121 CTGCCAGCTGTGAGTGTGCCACGCCCAAGAGATACAGGTGCCAGAAAGTCTGC 177

RESULT 6  
US-10-112-267-17  
Sequence 17, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/10/112,267  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 17  
LENGTH: 1734

TYPE: DNA  
ORGANISM: Mus musculus  
US-10-112-267-17

Query Match  
Best Local Similarity 100.0%; Score 90; DB 15; Length 1734;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGACGAGGAGTCTGCGACACCTGATGTCTGGACCCAGCCA 469  
|||||  
DB 418 AGTGTGTGACGAGGAGTCTGCGACACCTGATGTCTGGACCCAGCCA 477

QY 470 GGGCCTGTTGTGACCTGGGGGAGGCC 499  
|||||  
DB 478 GGGCCTGTTGTGACCTGGGGGAGGCC 507

RESULT 7  
US-10-112-267-18/c  
Sequence 18, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:

APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P117682  
CURRENT APPLICATION NUMBER: US/10/112,267

PRIOR APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 18  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-112-267-18

Query Match  
Best Local Similarity 100.0%; Score 90; DB 15; Length 1734;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGACGAGGAGTCTGCGACACCTGATGTCTGGACCCAGCCA 469  
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DB 1317 AGTGTGTGACGAGGAGTCTGCGACACCTGATGTCTGGACCCAGCCA 1258

QY 470 GGGCCTGTTGTGACCTGGGGGAGGCC 499  
|||||  
DB 1257 GGGCCTGTTGTGACCTGGGGGAGGCC 1228

RESULT 8  
US-10-010-408-10  
Sequence 10, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castellot, Jr.  
TITLE OF INVENTION: NO. US20020165185A1e1 Heparin-Induced CCN-like Molecules  
and Uses Therefor  
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998

APPLICATION NUMBER: <unknown>  
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEX: (617)742-4214

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:

LENGTH: 174 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 1..174

SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-010-408-10

Query Match  
Best Local Similarity 6.7%; Score 59; DB 15; Length 174;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 825 CCTGTCCAAATTGAGACACAGCCCTGCTCAACCACTGTGGCTGGGCAT 883  
|||||  
DB 1 CCTGTCCAAATTGAGACACAGCCCTGCTCAACCACTGTGGCTGGGCAT 59

RESULT 9  
US-09-864-761-23432  
Sequence 23432, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aecmics-X-1

CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 23432  
LENGTH: 199  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL139352.8  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7  
OTHER INFORMATION: NT HIT: AF083500.1, EVALUO 1.00e-108  
OTHER INFORMATION: SWISSPROT HIT: O19113, EVALUO 9.00e-19  
US-09-864-761-23432

Query Match 3.6%; Score 32; DB 10; Length 199;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GAGGATGTGGCGCTGCCAGCTGGACTGCC 685  
|||||  
DB 129 GAGGATGTGGCGCTGCCAGCTGGACTGCC 160  
RESULT 10  
US-09-864-761-6698  
Sequence 6698, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeonica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 6698  
LENGTH: 586  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL139352.8  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7  
US-09-864-761-6698

Query Match 3.6%; Score 32; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GAGGATGTGGCGCTGCCAGCTGGACTGCC 685  
|||||  
DB 342 GAGGATGTGGCGCTGCCAGCTGGACTGCC 373  
RESULT 11  
US-10-112-267-38  
Sequence 38, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane

APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/10/112,267  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 38  
LENGTH: 738  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-112-267-38

Query Match 3.6% Score 32: DB 15: Length 738;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 32: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GTACCCCTGCTGCTGATGCTGCTGCTGCTG 406  
DB 115 GTACCCCTGCTGCTGATGCTGCTGCTGCTG 146

RESULT 12  
US-10-112-267-39  
Sequence 39, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Bolstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/10/112,267  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 39  
LENGTH: 841  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1-841  
OTHER INFORMATION: Sequence is synthesized.  
US-10-112-267-39

Query Match 3.6% Score 32: DB 15: Length 841;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;

Matches 32: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 654 GAGGATGTGGGCTGCCAGCTGGAGCTGCC 685

DB 417 GAGGATGTGGGCTGCCAGCTGGAGCTGCC 448  
RESULT 13  
US-10-137-866-319  
Sequence 319, Application US/10137866  
Publication No. US20030129689A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C151  
CURRENT APPLICATION NUMBER: US/10/137,866  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059836  
PRIOR FILING DATE: 1997-09-24  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062285  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062814  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063550  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063561  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063704  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063733  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063735  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063738  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064248  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064809  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066453  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069212  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069278  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069334  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069694  
PRIOR FILING DATE: 1997-12-16  
PRIOR APPLICATION NUMBER: 60/072320  
PRIOR FILING DATE: 1998-01-23  
PRIOR APPLICATION NUMBER: 60/073612  
PRIOR FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: 60/074086  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/074092  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081695  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081818  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082999  
PRIOR FILING DATE: 1998-04-24  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083545

PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085149  
PRIOR FILING DATE: 1998-05-12  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086414  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/086430  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088730  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088741  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090538  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091982

Query Match 3.6%; Score 32; DB 14; Length 1266;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCGTGCTGATGCTGTGCTGCTG 406  
|||||  
Db 136 GTACCCGTGCTGATGCTGTGCTGCTG 167

RESULT 14  
US-10-146-726-319  
; Sequence 319, Application US/10146726

```
; Publication No. US20030129690A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenlin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C308
; CURRENT APPLICATION NUMBER: US/10/146,726
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-726-319
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Query Match          3.6%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      375 GTACCCCTGTGCTGATGCTGTGCTGCTG 406
          |||||||
DB      136 GTACCCCTGTGCTGATGCTGTGCTGCTG 167
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RESULT 15
US-10-146-727-319
; Sequence 319, Application US/10146727
; Publication No. US20030129691A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenlin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C312
; CURRENT APPLICATION NUMBER: US/10/146,727
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
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; ORGANISM: Homo Sapien
US-10-146-727-319
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Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      375 GTACCCCTGTGCTGATGCTGTGCTGCTG 406
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DB      136 GTACCCCTGTGCTGATGCTGTGCTGCTG 167
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Search completed: July 28, 2003, 15:36:31
Job time : 217.455 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:16:26 ; Search time 1566.4 Seconds  
(without alignments)  
9129.604 Million cell updates/sec

Title: US-10-010-408-1\_COPY\_1\_883  
Perfect score: 883  
Sequence: 1 GACGCTCTGATCTCCAGAG.....ACCACTGTGGGTGGCAT 883

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	10.2	940	14	B0937887
2	67	7.6	537	14	B0560868
3	49	5.5	424	10	BB849097
4	32	3.6	380	12	B6900020
5	32	3.6	405	12	B6900069
6	32	3.6	489	14	BM751866

7	32	3.6	618	12	B6538695
8	32	3.6	620	13	B6928868
9	32	3.6	651	13	B1457141
10	32	3.6	749	9	AL555144
11	32	3.6	750	13	BM043988
12	32	3.6	790	13	BM046275
13	32	3.6	886	13	B1826781
14	32	3.6	886	13	B1822142
15	32	3.6	888	13	B1825652
16	32	3.6	916	13	B1457367
17	32	3.6	928	13	B1161474
18	32	3.6	933	14	B0278961
19	32	3.6	979	14	B0279131
20	32	3.6	1006	14	BM921531
21	32	3.6	1022	14	B0952960
22	32	3.6	1058	14	BM805088
23	32	3.6	1073	14	B0073722
24	32	3.6	1166	13	BM543799
25	32	3.6	1251	14	B0961357
26	30	3.4	190	9	AA647775
27	23	2.6	436	17	A0095651
28	23	2.6	742	13	B1758148
29	23	2.6	792	13	B1823598
30	23	2.6	966	12	BF141695
31	21	2.4	495	13	B1204749
32	21	2.4	529	9	A1897896
33	21	2.4	561	12	BF051668
34	21	2.4	563	9	A1897344
35	21	2.4	609	9	AL485142
36	21	2.4	620	10	AW223381
37	20	2.3	188	14	H55466
38	20	2.3	232	9	AL658941
39	20	2.3	251	9	AT303895
40	20	2.3	288	10	BE574058
41	20	2.3	319	13	BM389674
42	20	2.3	332	17	AZ650040
43	20	2.3	334	14	BM698298
44	20	2.3	372	12	BF918366
45	20	2.3	381	10	BE573338

## ALIGNMENTS

RESULT 1  
LOCUS B0937887 940 bp mRNA linear EST 21-AUG-2002  
DEFINITION AGENCOURT\_8951807 NCI CGAP Co24 Mus musculus cDNA clone  
IMAGE:6476852 5', mRNA sequence.  
ACCESSION B0937887  
VERSION B0937887.1 GI:22353365  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 940)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM14017 row: n column: 21  
High quality sequence stop: 543.  
location/Qualifiers  
1. 940

/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone\_image="6476852"  
/clone\_lib="NCI\_CGAP\_CO24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: pGEM-SPOrt6; Site.1: NotI;  
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 169 a 277 c 288 g 200 t 6 others  
ORIGIN

Query Match 10.2%; Score 90; DB 14; Length 940;  
Best Local Similarity 100.0%; Pred. No. 9,6e-31;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 410 AGGTGTGCACGGAGCTGGGGAGTCGCGACACGTCATGTCTGCACCCAGCCA 469  
|||||  
Db 444 AGGTGTGCACGGAGCTGGGGAGTCGCGACACGTCATGTCTGCACCCAGCCA 503  
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Qy 470 GGGCTGTGTTTTCAGCTGGGGAGCC 499  
|||||  
Db 504 GGGCTGTGTTTTCAGCTGGGGAGCC 533  
|||||

RESULT 2  
B0560868 537 bp mRNA linear EST 20-JUN-2002  
LOCUS H4067A01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone  
DEFINITION H4067A01-5', mRNA sequence.  
ACCESSION B0560868  
VERSION B0560868.1 GI:21461753  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 537)  
VanBuren,V., Plao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin  
P.R., Stegg,C.A., Baasey,U., Alba,K., Hamatani,T., Kargul,G.J.,  
Luo,A.G. and Ko,M.S.H.  
Assembly, verification, and initial annotation of NIA 7.4K mouse  
cDNA clone set  
Unpublished (2002)  
JOURNAL Contact: Yong Qian  
COMMENT Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
This clone set has been freely distributed to the community. Please  
visit [http://igsun.grc.nia.nih.gov/cDNA/NIA\\_7\\_4K.html](http://igsun.grc.nia.nih.gov/cDNA/NIA_7_4K.html) for details.  
Plate: H4067 row: A column: 01  
Seq primer: -21M13 Reverse  
High quality sequence stop: 537  
POLYA-No.

FEATURES  
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1..537  
/organism="Mus musculus"  
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/clone\_lib="NIA Mouse 7.4K cDNA Clone Set"  
/sex="mixed"  
/dev\_stage="mixed"  
/lab\_host="DH10B"  
/note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; This  
clone is among a rearranged set of 7,407 clones from more  
than 20 cDNA libraries."  
BASE COUNT 87 a 162 c 166 g 122 t  
ORIGIN

Query Match 7.6%; Score 67; DB 14; Length 537;  
Best Local Similarity 100.0%; Pred. No. 3,8e-20;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 410 AGGTGTGCACGGAGCTGGGGAGTCGCGACACGTCATGTCTGCACCCAGCCA 469  
|||||  
Db 471 AGGTGTGCACGGAGCTGGGGAGTCGCGACACGTCATGTCTGCACCCAGCCA 530  
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Qy 470 GGGCTGTG 476  
|||||  
Db 531 GGGCTGTG 537  
|||||

RESULT 3  
BB849097 424 bp mRNA linear EST 26-NOV-2001  
LOCUS BB849097 RIKEN full-length enriched, adult inner ear Mus musculus  
DEFINITION BB849097 RIKEN full-length enriched, adult inner ear Mus musculus  
CDNA clone F930006602 5', mRNA sequence.  
ACCESSION BB849097  
VERSION BB849097.1 GI:17090551  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 424)  
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,  
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii  
Y., Ito,M., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Matsuyama,T.,  
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,  
Saito,K., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,  
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa  
A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,  
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.  
2001)

TITLE Unpublished (2001)  
JOURNAL Contact: Yoshinori Hayashizaki  
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.c.riken.go.jp,  
URL:<http://genome.gsc.riken.go.jp/>  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura  
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.  
e mouse tissues.

FEATURES  
source Location/Qualifiers  
1..424  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="F930006602"  
/clone\_lib="RIKEN full-length enriched, adult inner ear"

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/tissue_type="inner ear"
/dev_stage="adult"
/note="pooled tissues : (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"
BASE COUNT      65 a      124 c      132 g      103 t
ORIGIN

Query Match      5.5%; Score 49; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGACGAGGAGGAGGAGTCTCGACACCACTGCTGTCTGC 458
DB 373 AGTGTGTGACGAGGAGGAGGAGTCTCGACACCACTGCTGTCTGC 421

RESULT 4
BG900020      380 bp      mRNA      linear      EST 06-NOV-2001
LOCUS      HOA48-1-G2.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA
DEFINITION      , mRNA sequence.
ACCESSION      BG900020
VERSION      BG900020.1 GI:14310269
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 380)
AUTHORS      Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE      Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
JOURNAL
MEDLINE
COMMENT      Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: 47.

FEATURES
source      Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="Cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
BASE COUNT      58 a      139 c      118 g      65 t
ORIGIN

Query Match      3.6%; Score 32; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGTGATGCTGTGCTGCTG 406
DB 206 GTACCCCTGTGCTGTGATGCTGTGCTGCTG 237

RESULT 5
BG900069      405 bp      mRNA      linear      EST 06-NOV-2001
LOCUS      HOA51-1-A11.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
DEFINITION      cDNA, mRNA sequence.
ACCESSION      BG900069
VERSION      BG900069.1 GI:14310318
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 405)
AUTHORS      Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE      Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
JOURNAL
MEDLINE
COMMENT      Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: 47.

FEATURES
source      Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="Cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
BASE COUNT      62 a      140 c      135 g      68 t
ORIGIN

Query Match      3.6%; Score 32; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGTGATGCTGTGCTGCTG 406
DB 202 GTACCCCTGTGCTGTGATGCTGTGCTGCTG 233

RESULT 6
BM751866      489 bp      mRNA      linear      EST 04-MAR-2002
LOCUS      K-EST0028180 S2SN0668S1 Homo sapiens cDNA clone S2SN0668S1-2-D09
DEFINITION      5', mRNA sequence.
ACCESSION      BM751866
VERSION      BM751866.1 GI:19081484
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 489)
AUTHORS      Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL
COMMENT      Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr

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Plate: 2 row: D column: 09  
High quality sequence stop: 489.  
Location/Qualifiers  
1. 489

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="S2SN06851-2-D09"  
/clone\_lib="S2SN06851"  
/sex="M"  
/tissue\_type="Ascites"  
/cell\_type="Epithelial"  
/cell\_line="SNU-668"  
/lab\_host="TOP10F"

/note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI; Site\_2: NotI; The poly (A)+ RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli TOP10F by electroporation method. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli TOP10F with electroporation method."

BASE COUNT 75 a 173 c 159 g 82 t

Query Match 3.6%; Score 32; DB 14; Length 489;  
Best Local Similarity 100.0%; Pred. No. 0.0006;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 654 GAGGATGTCGGCTGCCAGCTGGACTGCC 685

Db 139 GAGGATGTCGGCTGCCAGCTGGACTGCC 170

RESULT 7 618 bp mRNA linear EST 03-APR-2001  
BG538695  
LOCUS 602566932F1 NIH\_MGC\_77 Homo sapiens cDNA, clone IMAGE:4691574 5',  
DEFINITION mRNA sequence.

ACCESSION BG538695  
VERSION BG538695.1 GI:13530928

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 7

AUTHORS NIH-MGC

TITLE NIH-MGC

JOURNAL

COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCM510 row: P column: 07  
High quality sequence stop: 499.  
Location/Qualifiers

1. 618  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4691574"  
/clone\_lib="NIH\_MGC\_77"  
/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcgctcgcc); Site\_2: SfiI (ggccatctggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

BASE COUNT 95 a 194 c 213 g 116 t

Query Match 3.6%; Score 32; DB 12; Length 618;  
Best Local Similarity 100.0%; Pred. No. 0.00063;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCCTGTCGTGATGCTGCTGCTG 406

Db 291 GTACCCCTGTCGTGATGCTGCTGCTG 322

RESULT 8

LOCUS BG928868

DEFINITION HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

ACCESSION BG928868

VERSION BG928868.1 GI:14323391

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 8

AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.

TITLE Identification and initial characterization of 5000 expressed

JOURNAL sequenced tags (ESTs) each from adult human normal and

MEDLINE osteoarthritic cartilage cDNA libraries

COMMENT 21482651

Contact: Sanjay Kumar

UM2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay\_kumar-1@sk.com

Seq primer: 77.

Location/Qualifiers  
1. 620  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/tissue\_type="Cartilage"  
/lab\_host="E.coli DH10 B"  
/note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI; Directional"

BASE COUNT 97 a 218 c 207 g 98 t

Query Match 3.6%; Score 32; DB 13; Length 620;  
 Best Local Similarity 100.0%; Pred. No. 0.00063;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGCTGCTG 406  
 ||||||||||||||||||||||||||||||||  
 Db 210 GTACCCCTGCTGCTGATGGCTGCTGCTG 241

RESULT 9  
 LOCUS B1457141 651 bp mRNA linear EST 21-AUG-2001  
 DEFINITION 603185392F1 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:5258159 5',  
 mRNA sequence.  
 ACCESSION B1457141  
 VERSION B1457141.1 GI:15247797  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 651)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM1869 row: 9 column: 24  
 High quality sequence stop: 651.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5258159"  
 /clone\_1ib="NIH\_MGC\_42"  
 /tissue\_type="epithelioid carcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH-MGC Library. |"

BASE COUNT 91 a 230 c 219 g 111 t

ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 651;  
 Best Local Similarity 100.0%; Pred. No. 0.00063;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGCTGCTG 406  
 ||||||||||||||||||||||||||||||||  
 Db 96 GTACCCCTGCTGCTGATGGCTGCTGCTG 127

RESULT 10  
 LOCUS AL555144 749 bp mRNA linear EST 16-FEB-2001  
 DEFINITION AL555144 LTI\_NFL006\_P12 Homo sapiens cDNA clone CSODK0071021 5  
 prime, mRNA sequence.  
 ACCESSION AL555144  
 VERSION AL555144.1 GI:12896595

KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 749)  
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

FEATURES  
 source  
 1..749  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CSODK0071021"  
 /clone\_1ib="LTI\_NFL006\_P12"  
 /tissue\_type="Placenta"  
 /note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed by  
 Life Technologies. Contact: Feng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : [li.f@length.invitrogen.com](mailto:li.f@length.invitrogen.com)"

BASE COUNT 128 a 252 c 236 g 133 t

ORIGIN

Query Match 3.6%; Score 32; DB 9; Length 749;  
 Best Local Similarity 100.0%; Pred. No. 0.00065;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGCTGCTG 406  
 ||||||||||||||||||||||||||||||||  
 Db 432 GTACCCCTGCTGCTGATGGCTGCTGCTG 463

RESULT 11  
 LOCUS BM043988 750 bp mRNA linear EST 07-NOV-2001  
 DEFINITION BM043988 603620978F1 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:3446794 5',  
 mRNA sequence.  
 ACCESSION BM043988  
 VERSION BM043988.1 GI:16773255  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 750)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCTD/DRP  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM1929 row: k column: 19  
 High quality sequence stop: 714.  
 Location/Qualifiers  
 1..750  
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 /db\_xref="taxon:9606"

/clone\_11b="NIH\_MGC\_40"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: prostate; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

BASE COUNT  
ORIGIN

112 a 267 c 246 g 125 t

Query Match 3.6%; Score 32; DB 13; Length 750;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GRACCCCTGCTGCTGATGCTGCTGCTG 406  
Db 142 GRACCCCTGCTGCTGATGCTGCTGCTG 173

RESULT 12  
BM046275 790 bp mRNA linear EST 07-NOV-2001  
LOCUS 603626068F1 NIH\_MGC\_40 Homo sapiens CDNA clone IMAGE:5452480 5',  
DEFINITION mRNA sequence.  
ACCESSION BM046275  
VERSION BM046275.1 GI:16775542  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 790)  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM1944 row: h column: 17  
High quality sequence stop: 780.  
Location/Qualifiers

FEATURES  
source

1. 790  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_11b="NIH\_MGC\_40"  
/clone\_11b="NIH\_MGC\_40"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: prostate; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

BASE COUNT  
ORIGIN

121 a 265 c 269 g 135 t

Query Match 3.6%; Score 32; DB 13; Length 790;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 654 GAGGATGCGCGTGGCCAGCTGGACTGCC 685  
Db 265 GAGGATGCGCGTGGCCAGCTGGACTGCC 296

RESULT 13  
B1826781 800 bp mRNA linear EST 04-OCT-2001  
LOCUS 603077268F1 NIH\_MGC\_119 Homo sapiens CDNA clone IMAGE:5180650 5',  
DEFINITION mRNA sequence.  
ACCESSION B1826781  
VERSION B1826781.1 GI:15938331  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 800)  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM1420 row: g column: 18  
High quality sequence stop: 788.  
Location/Qualifiers

FEATURES  
source

1. 800  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_11b="NIH\_MGC\_119"  
/clone\_11b="NIH\_MGC\_119"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC library."

BASE COUNT 115 a 284 c 264 g 136 t 1 others

Query Match 3.6%; Score 32; DB 13; Length 800;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GRACCCCTGCTGCTGATGCTGCTGCTG 406  
Db 120 GRACCCCTGCTGCTGATGCTGCTGCTG 151

RESULT 14  
B1822142 886 bp mRNA linear EST 04-OCT-2001  
LOCUS 603039845F1 NIH\_MGC\_115 Homo sapiens CDNA clone IMAGE:5180650 5',  
DEFINITION mRNA sequence.  
ACCESSION B1822142  
VERSION B1822142.1 GI:15933692  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Query Match 3.6%; Score 32; DB 13; Length 800;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 886)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: L1A11450 row: j column: 11  
High quality sequence stop: 865.

FEATURES  
Source  
1..886  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5180650"  
/clone\_lib="NIH\_MGC\_115"  
/lab\_host="DH10B"  
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

BASE COUNT 134 a 310 c 288 g 154 t  
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 886;  
Best Local Similarity 100.0%; Pred. No. 0.00067;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GTACCCCTGCTGCTGATGCTGCTGCTG 406  
|||  
Db 121 GTACCCCTGCTGCTGATGCTGCTGCTG 152

RESULT 15  
BI825652 888 bp mRNA linear EST 04-OCT-2001  
LOCUS 603072631f1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5164614 5',  
DEFINITION mRNA sequence.  
ACCESSION BI825652  
VERSION BI825652.1 GI:15937202  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 888)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: L1A11408 row: n column: 07  
High quality sequence stop: 877.  
Location/Qualifiers

FEATURES

source

1..888  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5164614"  
/clone\_lib="NIH\_MGC\_119"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."

BASE COUNT 130 a 308 c 288 g 162 t  
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 888;  
Best Local Similarity 100.0%; Pred. No. 0.00067;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GTACCCCTGCTGCTGATGCTGCTGCTG 406  
|||  
Db 117 GTACCCCTGCTGCTGATGCTGCTGCTG 148

Search completed: July 28, 2003, 18:02:04  
Job time : 1568.4 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:19:16 ; Search time 2092.59 Seconds

(without alignments)  
10472.371 Million cell updates/sec

Title: US-10-010-408-3

Perfect score: 753  
Sequence: 1 ATGAGGGGAGCCCGACTGAT.....CATGGAACAGCTCTTCTAA 753Scoring table: OLIGO\_MNC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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GenEmbl:.*
1: gb_ba:.*
2: gb_htg:.*
3: gb_in:.*
4: gb_ov:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_ba:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_mu:.*
20: em_om:.*
21: em_or:.*
22: em_ov:.*
23: em_pat:.*
24: em_ph:.*
25: em_pl:.*
26: em_ro:.*
27: em_sts:.*
28: em_un:.*
29: em_vl:.*
30: em_htg_hum:.*
31: em_htg_inv:.*
32: em_htg_other:.*
33: em_htg_mus:.*
34: em_htg_pln:.*
35: em_htg_rnd:.*
36: em_htg_rnd:.*
37: em_htg_vit:.*
38: em_sy:.*
39: em_htgo_hum:.*
40: em_htgo_mus:.*
41: em_htgo_other:.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	235	31.2	1741	10	AF259981	AF259981 Rattus no
2	223	29.6	137964	2	AC126895	AC126895 Rattus no
3	223	29.6	226303	2	AC095418	AC095418 Rattus no
4	154	20.5	137964	2	AC126895	AC126895 Rattus no
5	90	12.0	1734	6	AR210324	AR210324 Sequence
6	90	12.0	1734	6	AR210325	AR210325 Sequence
7	90	12.0	1734	10	AF100778	AF100778 Mus muscu
8	90	12.0	61072	10	AL731698	AL731698 Mouse DNA
9	90	12.0	216757	2	AL669906	AL669906 Mus muscu
10	80	10.6	1739	10	AF126063	AF126063 Mus muscu
11	32	4.2	738	6	AR210337	AR210337 Sequence
12	32	4.2	841	6	AR210338	AR210338 Sequence
13	32	4.2	1266	6	AX076919	AX076919 Sequence
14	32	4.2	1266	6	AX464186	AX464186 Sequence
15	32	4.2	1283	9	AF083500	AF083500 Homo sapi
16	32	4.2	1293	6	AR210322	AR210322 Sequence
17	32	4.2	1293	6	AR210323	AR210323 Sequence
18	32	4.2	1309	9	AF074604	AF074604 Homo sapi
19	32	4.2	1427	9	AF100780	AF100780 Homo sapi
20	32	4.2	1450	9	BC017782	BC017782 Homo sapi
21	32	4.2	107260	9	AL139352	AL139352 Human DNA
22	27	3.6	51	6	AR210371	AR210371 Sequence
23	27	3.6	51	6	AX076923	AX076923 Sequence
24	22	2.9	99395	2	AC010446	AC010446 Homo sapi
25	22	2.9	149483	2	AC110904	AC110904 Mus muscu
26	22	2.9	180464	2	AC116351	AC116351 Homo sapi
27	22	2.9	200050	1	AL646068	AL646068 Rattus no
28	21	2.8	66908	2	AC119914	AC119914 Mus muscu
29	21	2.8	150944	2	AC112856	AC112856 Rattus no
30	21	2.8	181343	10	AL671882	AL671882 Mouse DNA
31	21	2.8	204937	2	AL831741	AL831741 Mus muscu
32	21	2.8	215105	2	AC073717	AC073717 Mus muscu
33	21	2.7	1003	5	CHKTCEAA	CHKTCEAA Chicken T-C
34	20	2.7	1200	6	AX122384	AX122384 Sequence
35	20	2.7	1221	9	HSX801506	AX113637 Homo sapi
36	20	2.7	1481	8	AB033535	AB033535 Oryza sat
37	20	2.7	3301	9	BC019257	BC019257 Homo sapi
38	20	2.7	4467	9	AB020659	AB020659 Homo sapi
39	20	2.7	7172	10	AB008516	AB008516 Mus muscu
40	20	2.7	36296	9	HSEB1G9	282180 Human DNA s
41	20	2.7	83021	2	AC095541	AC095541 Rattus no
42	20	2.7	84001	9	AL162739	AL162739 Human DNA
43	20	2.7	92458	9	AL353715	AL353715 Human DNA
44	20	2.7	114793	9	AF217796	AF217796 Homo sapi
45	20	2.7	117840	9	AL162400	AL162400 Human DNA

## ALIGNMENTS

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RESULT 1
AF259981
LOCUS
DEFINITION
Rattus norvegicus CCN family protein COP-1 (COP-1) mRNA, complete
cds.
ACCESSION
AF259981
VERSION
AF259981.1 GI:7739780
KEYWORDS
ORGANISM
Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 1741)
Zhang, R., Averboukh, L., Zhu, W., Zhang, H., Jo, H., Dempsey, P. J.,
```

TITLE Coffey R.J., Pardee A.B. and Liang P.  
 Identification of rCop-1, a new member of the CCN protein family,  
 as a negative regulator for cell transformation  
 JOURNAL Mol. Cell. Biol. 18 (10), 6131-6141 (1998)  
 MEDLINE 98414629  
 PUBMED 9742130  
 REFERENCE 2 (bases 1 to 1741)  
 AUTHORS Liang, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer Center, 649 MRB II, Nashville, TN 37232, USA  
 FEATURES  
 source Location/Qualifiers  
 1. 1741  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 1. 1741  
 /gene="Cop-1"  
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 WYCDGVPAIDRSAAQGHQSLALVTPASADPMPMWSAMGAPCSTGCTGATATVSN  
 ONRFGLEORLCLPRCLAAHSNSNSAF"  
 BASE COUNT 386 a 491 c 480 g 384 t  
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 Query Match 31.2%; Score 235; DB 10; Length 1741;  
 Best Local Similarity 99.4%; Pred. No. 1.6e-116;  
 Matches 335; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 417 GGTGGCCAGCTGGAGCTGCCAGCCGCCCAAGAGATACGTCGACGAGAAATGCTGCC 476  
 DB 678 GTGTGCCAGCTGGAGCTGCCAGCCGCCCAAGAGATACGTCGACGAGAAATGCTGCC 737  
 QY 477 CGAGTGGATATGACCAAGAGAGTACACCGCGCATCCAGCGCTCCAGCGCCCAAGAGACA 536  
 DB 738 CGAGTGGATATGACCAAGAGAGTACACCGCGCATCCAGCGCTCCAGCGCCCAAGAGACA 797  
 QY 537 CCAACTTCTGCGCTTGTCTACTCTGCTGCTGATGAGTCCCTTGTCCAAATTGAGAGAC 596  
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 DB 918 GAACGATTTCTGCCAAGTGGAGATCCAAAGCGCGCTGTGTCTGGCCAGACCTGCTGGC 977  
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 DB 978 AGCCAGAGCCACAGCTCATGGAGACAGTCTTTCTTA 1014  
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 DEFINITION \*\*\* 49 unordered pieces.  
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 VERSION AC126895.1  
 KEYWORDS HTG; HTGS\_PHASE1.  
 SOURCE Rattus norvegicus.  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE  
AUTHORS

Rattus.  
 1 (bases 1 to 137964)  
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-oshman, F.R., Allen, C.,  
 Alsbrooks, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T.,  
 Barbara, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,  
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 Direct Submission  
 Unpublished  
 2 (bases 1 to 137964)  
 Worley, K.C.  
 Direct Submission  
 Submitted (10-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 137964)  
 Worley, K.C.  
 Direct Submission  
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: G2HG  
 Center clone name: CH230-301E4  
 ----- Summary Statistics  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 89474 bases at least Q40  
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 Consensus quality: 96506 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length

(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 49 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
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## FEATURES

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/db\_xref="taxon:10116"  
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## RESULT 3

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Rattus norvegicus clone CH230-7C10, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
51 unordered pieces.

## ACCESSION

AC095418  
AC095418.3 GI:21717893

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

HTG: HTGS\_PHASE1.  
Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
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1 (bases 1 to 226303)  
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Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S.,  
Williams,G., Williamson,A., Wlarczyk,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,  
Wetstock,G. and Gibbs,R.  
Direct Submission  
Unpublished  
2 (bases 1 to 226303)  
Worley,K.C.  
Direct Submission  
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 226303)  
Worley,K.C.  
Direct Submission  
Submitted (11-JUN-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 10, 2002 this sequence version replaced gi:17941885.  
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Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
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Project Information  
Center project name: GCDF  
Center clone name: CH230-7C10  
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Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 185950 bases at least 940  
Consensus quality: 190362 bases at least 930  
Consensus quality: 193076 bases at least 920

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 51 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1051: contig of 1051 bp in length  
1052 1151: gap of unknown length  
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DB 112254 AGGACACCACTTTTGGCCCTTGTCACCTGCTGCTGATGCTCTGTCGCAAAATTG 112313
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OY 591 GAGCAGACCTGGGGGCCCTGCTCAACCACTGTGGGTGGGATAGGCACCCGAGTGTG 650
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DB 112314 GAGCAGACCTGGGGGCCCTGCTCAACCACTGTGGGTGGGACANAGCACCCGAGTGTG 112373
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OY 651 CAACCAAGAACGATTCTGCCAAGTGAATTCACACGCCGCTGTGTCTGCCAGACCTTG 710
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DB 112374 CAACCAAGAACGATTCTGCCAAGTGAATTCACACGCCGCTGTGTCTGCCAGACCTTG 112433
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OY 711 CCTGGACAGCAGAGCAGCTCATGTGAACAGTCTTTCTTAA 753
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DB 112434 CCTGGACAGCAGAGCAGCTCATGTGAACAGTCTTTCTTAA 112476
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VERSION  
AC126895.1 GI:21724040  
HTG: HTGS\_PHASE1.  
Rattus norvegicus.  
Rattus norvegicus  
Rattus norvegicus  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 137964)  
REFERENCE  
Munry, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F., Allen, C., Albrooks, S.L., Amaralunge, H.C., Are, J.R., Ayale, M., Banks, T., Barbara, J., Benton, J., Blinige, K., Blumenthal, K., Bonin, D., Bouck, J., Bowe, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chaco, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Datome, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escoto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J., H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulik, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovach, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Louised, H., Lozadro, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, S., Nguyen, N., Nickerson, E., Nwokkenko, S., Ogum, M., Okunolu, G., Ogunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Plickens, R., Plinius, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshart, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umanai, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleciyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Glibbs, R.  
Weinstock, G. and Glibbs, R.  
Direct Submission  
Unpublished  
2 (bases 1 to 137964)  
Worley, K.C.  
Direct Submission  
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 137964)  
Worley, K.C.  
Direct Submission  
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GZHG  
Center clone name: CH230-301E4  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye 100% of reads

RESULT 4  
AC126895/c 137964 bp DNA linear HTG 24-JUL-2002  
LOCUS Rattus norvegicus clone CH230-301E4, \*\*\* SEQUENCING IN PROGRESS  
DEFINITION \*\*\* 48 unordered pieces.  
ACCESSION AC126895

Assembly program: Phrap; version 0.990329  
Consensus quality: 894/74 bases at least Q40  
Consensus quality: 93422 bases at least Q30  
Consensus quality: 96506 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 49 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1056: contig of 1056 bp in length  
1057 1156: gap of unknown length  
1157 2335: contig of 1179 bp in length  
2336 2435: gap of unknown length  
2436 3442: contig of 1007 bp in length  
3443 3543: gap of unknown length  
3543 5081: contig of 1539 bp in length  
5082 5181: gap of unknown length  
5182 6424: contig of 1243 bp in length  
6425 6524: gap of unknown length  
6525 7814: contig of 1290 bp in length  
7815 7914: gap of unknown length  
7915 9153: contig of 1239 bp in length  
9154 9253: gap of unknown length  
9254 10445: contig of 1192 bp in length  
10446 10545: gap of unknown length  
10546 11771: contig of 1226 bp in length  
11772 11871: gap of unknown length  
11872 13240: contig of 1369 bp in length  
13241 13340: gap of unknown length  
13341 14359: contig of 1019 bp in length  
14360 14459: gap of unknown length  
14460 15551: contig of 1192 bp in length  
15552 15751: gap of unknown length  
15752 17494: contig of 1743 bp in length  
17495 17594: gap of unknown length  
17595 18679: contig of 1085 bp in length  
18680 18779: gap of unknown length  
18780 20681: contig of 1902 bp in length  
20682 22118: contig of 1337 bp in length  
22119 22218: gap of unknown length  
22219 23578: contig of 1360 bp in length  
23579 23678: gap of unknown length  
23679 25423: contig of 1745 bp in length  
25424 25523: gap of unknown length  
25524 27808: contig of 2285 bp in length  
27809 27908: gap of unknown length  
27909 30272: contig of 2364 bp in length  
30273 30372: gap of unknown length  
30373 33091: contig of 2719 bp in length  
33092 33191: gap of unknown length  
33192 35777: contig of 2586 bp in length  
35778 35877: gap of unknown length  
35878 36908: contig of 1031 bp in length  
36909 37008: gap of unknown length  
37009 38930: contig of 1922 bp in length  
38931 39030: gap of unknown length  
39031 41210: contig of 2180 bp in length  
41211 41310: gap of unknown length  
41311 42937: contig of 1627 bp in length  
42938 43037: gap of unknown length  
43038 46120: contig of 3083 bp in length  
46121 46220: gap of unknown length  
46221 48217: contig of 1997 bp in length  
48218 48317: gap of unknown length  
48319 50433: contig of 2116 bp in length  
50434 50533: gap of unknown length

50534 52880: contig of 2347 bp in length  
52881 52980: gap of unknown length  
52981 55194: contig of 2214 bp in length  
55195 55294: gap of unknown length  
55295 57482: contig of 2188 bp in length  
57483 57582: gap of unknown length  
57583 60781: contig of 319 bp in length  
60782 60882: gap of unknown length  
60882 62599: contig of 1718 bp in length  
62600 62699: gap of unknown length  
62700 65200: contig of 2504 bp in length  
65200 65303: gap of unknown length  
65304 66314: contig of 1611 bp in length  
66315 67015: gap of unknown length  
67015 70839: contig of 3825 bp in length  
70840 70939: gap of unknown length  
70940 75139: contig of 4200 bp in length  
75140 75239: gap of unknown length  
75240 78296: contig of 3057 bp in length  
78297 78396: gap of unknown length  
78397 83138: contig of 4742 bp in length  
83139 83239: gap of unknown length  
83239 88204: contig of 4966 bp in length  
88205 88304: gap of unknown length  
88305 92238: contig of 3924 bp in length  
92239 92338: gap of unknown length  
92339 97339: contig of 5001 bp in length  
97340 97439: gap of unknown length  
97440 103534: contig of 6095 bp in length  
103535 103635: gap of unknown length  
103635 107080: contig of 3446 bp in length  
107081 107180: gap of unknown length  
107181 115201: contig of 8021 bp in length  
115202 115301: gap of unknown length  
115302 121237: contig of 5926 bp in length  
121238 121337: gap of unknown length  
121338 127910: contig of 6573 bp in length  
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Location/Qualifiers  
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/organism="Rattus norvegicus"  
/db\_xref="taxon:10116"  
/clone="CH230-301E4"  
BASE COUNT 31831 a 34027 c 35229 g 31979 t 4898 others  
ORIGIN  
Query Match 20.5%: Score 154; DB 2; Length 137964;  
Best Local Similarity 100.0%; Pred. No. 1.3e-72;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 278 TGGATGAGATGACGCTGCTGAGTGAATGCGCCGACGATGCTGATGAGAGACT 337  
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DB 77246 TGGATGAGATGACGCTGCTGAGTGAATGCGCCGACGATGCTGATGAGAGACT 77187  
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QY 338 TTAACCCAAATGACAGGCTCTGTCGCCGCTGATGAGCGTTCACCTCCGCCG 397  
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DB 77186 TTAACCCAAATGACAGGCTCTGTCGCCGCTGATGAGCGTTCACCTCCGCCG 77127  
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QY 398 TGTGAGTGAAGATGCGCGCTGCCAGCTGGCA 431  
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DB 77126 TGTGAGTGAAGATGCGCGCTGCCAGCTGGCA 77093  
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RESULT 5  
AR210324  
LOCUS AR210324 1734 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 17 from patent US 6387657.  
ACCESSION AR210324  
VERSION AR210324.1 GI:21512525  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 1734)  
AUTHORS Bostein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.  
TITLE WISP polypeptides and nucleic acids encoding same  
JOURNAL Patent: US 6387657-A 17 14-MAY-2002;  
FEATURES Location/Qualifiers  
source 1..1734  
/organism="unknown"  
BASE COUNT 355 a 491 c 495 g 393 t  
ORIGIN

Query Match 12.0%; Score 90; DB 6; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.8e-37;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 162 AGTGTGTCACGAGGCTGGGGAGTCTCTGGACCACTGATGTCGACCCAGCCA 221  
Db 418 AGTGTGTCACGAGGCTGGGGAGTCTCTGGACCACTGATGTCGACCCAGCCA 477

Oy 222 GGGCCTGGTTGTTCAGCCTGGGGGCGAGGCC 251  
Db 478 GGGCCTGGTTGTTCAGCCTGGGGGCGAGGCC 507

RESULT 6  
LOCUS AR210325/c 1734 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 18 from patent US 6387657.  
ACCESSION AR210325  
VERSION AR210325.1 GI:21512526  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1734)  
AUTHORS Bostein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.  
TITLE WISP polypeptides and nucleic acids encoding same  
JOURNAL Patent: US 6387657-A 18 14-MAY-2002;  
FEATURES Location/Qualifiers  
source 1..1734  
/organism="unknown"  
BASE COUNT 393 a 495 c 491 g 355 t  
ORIGIN

Query Match 12.0%; Score 90; DB 6; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.8e-37;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 162 AGTGTGTCACGAGGCTGGGGAGTCTCTGGACCACTGATGTCGACCCAGCCA 221  
Db 1317 AGTGTGTCACGAGGCTGGGGAGTCTCTGGACCACTGATGTCGACCCAGCCA 1258

Oy 222 GGGCCTGGTTGTTCAGCCTGGGGGCGAGGCC 251  
Db 1257 GGGCCTGGTTGTTCAGCCTGGGGGCGAGGCC 1228

RESULT 7  
LOCUS AF100778 1734 bp mRNA linear ROD 17-DEC-1998  
DEFINITION Mus musculus connective tissue growth factor related protein WISP-2 (Wisp2) mRNA, complete cds.  
ACCESSION AF100778  
VERSION AF100778.1 GI:4028578  
KEYWORDS  
SOURCE Mus musculus.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 1734)  
AUTHORS Pennica,D., Swanson,T.A., Welsh,J.W., Roy,M.A., Lawrence,D.A.,

Lee,J., Brush,J., Taneyhill,L.A., Denel,B., Lew,M., Matanabe,C., Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D., Hillan,K.J., Gurney,A.L., Bostein,D. and Levine,A.J.  
TITLE WISP genes are members of the connective tissue growth factor family that are up-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)  
MEDLINE 99061933  
PUBMED 9843955  
REFERENCE 2 (bases 1 to 1734)  
AUTHORS Pennica,D.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-1998) Molecular Oncology, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
FEATURES Location/Qualifiers  
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/cell\_line="C57MG"  
/cell\_type="epithelial"  
/tissue\_type="mammary"  
/note="Transformed by Wnt-1"  
1..1734  
/gene="Wisp2"  
257..1012  
/gene="Wisp2"  
/product="connective tissue growth factor related protein WISP-2"  
/protein\_id="AAC96320.1"  
/db\_xref="GI:4028579"  
/translation="MRGNPLHLIAISFICILSNVYSOLCPAPCAPMTPTPCPGVP LVLDCCGRCRCARLSECDHLVCPDSGLVQCPAGSGRAVCLFEEDSDCEY NGRRTLDGETFKPNCRVLCRDDGGFTCLPLCSDDVRLPSMDCPRPRIDVPGKCPB WCDQAVMOPAIOPSSAQGHQLSALVTPASADGFCPPMWSWTAMGCSYTCGLGATRS NONFCOLEIORLRLSRPCLASRSHSMSNAF"  
BASE COUNT 355 a 491 c 495 g 393 t  
ORIGIN

Query Match 12.0%; Score 90; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.8e-37;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 162 AGTGTGTCACGAGGCTGGGGAGTCTCTGGACCACTGATGTCGACCCAGCCA 221  
Db 418 AGTGTGTCACGAGGCTGGGGAGTCTCTGGACCACTGATGTCGACCCAGCCA 477

Oy 222 GGGCCTGGTTGTTCAGCCTGGGGGCGAGGCC 251  
Db 478 GGGCCTGGTTGTTCAGCCTGGGGGCGAGGCC 507

RESULT 8  
LOCUS AL731698 61072 bp DNA linear ROD 24-MAY-2002  
DEFINITION Mouse DNA sequence from clone Rp23-161B3 on chromosome 2, complete sequence.  
ACCESSION AL731698  
VERSION AL731698.10 GI:21214309  
KEYWORDS HTG.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 61072)  
AUTHORS Wallis,J.  
TITLE Direct Submission  
JOURNAL Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk On May 25, 2002 this sequence request was replaced g1:21213601. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations





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misc_feature 35071..39671
/note="assembly-fragment:03544
fragment_chain:1"
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/note="assembly-fragment:01438
fragment_chain:1"
misc_feature 46461..49809
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fragment_chain:2"
misc_feature 49910..54509
/note="assembly-fragment:00811
fragment_chain:2"
misc_feature 54610..65989
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clone_end:T7
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Query Match 12.0%; Score 90; DB 2; Length 216757;
Best Local Similarity 100.0%; Pred. No. 9.5e-38;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 162 AGTGTGACGAGGAGCTGGGGAGTCTGCGACACCTGCATGTCGAGACCCAGCA 221
DB 166450 AGTGTGTCACGAGGAGCTGGGGAGTCTGCGACACCTGCATGTCGAGACCCAGCA 166509
OY 222 GGGCTGGTTGTACAGCTGGGGAGGCCC 251
DB 166510 GGGCTGGTTGTACAGCTGGGGAGGCCC 166539
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LOCUS AF126063 1739 bp mRNA linear ROD 12-OCT-1999
DEFINITION Mus musculus connective tissue growth factor-like protein precursor
(cctgf) mRNA, complete cds.
ACCESSION AF126063
VERSION AF126063.1 GI:4337059
KEYWORDS
SOURCE
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1739)
Kumar,S., Hand,A.T., Connor,J.R., Dodds,R.A., Ryan,P.J.,
Trill,J.J., Fisher,S.M., Nuttall,M.E., Lipschutz,D.B., Zou,C.,
Hwang,S.M., Volta,B.J., James,I.E., Rieinan,D.J., Gowen,M. and
Lee,J.C.
TITLE Identification and cloning of a connective tissue growth
factor-like cDNA from human osteoblasts encoding a novel regulator
of osteoblast functions
JOURNAL J. Biol. Chem. 274 (24), 17123-17131 (1999)
MEDLINE 99287915
PUBMED 10358067
REFERENCE
2 (bases 1 to 1739)
Kumar,S. and Zou,C.
AUTHORS Direct Submission
TITLE Submitted (04-FEB-1999) Bone & Cartilage Biology, UW 2109,
Smithkline Beecham, 709 Swedeland Rd., King of Prussia, PA 19406,
USA
FEATURES
source
location/Qualifiers
1..1739
/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="Lung"
1..1739
/gene="Ctgef1"
242..997
/gene="Ctgef1"
/note="similar to the Mus musculus WISP-2 protein encoded
by the sequence presented in Genbank Accession Number
AF100778: putative growth factor: CTGF-L; contains IGF
binding (IGFBP), Von Willebrand factor type C (VWC) repeat
and thrombospondin type 1 (TSP1) domains; member of the
CCN (CTGF/Cyrl/Nov) family; lacks the fourth
carboxy-terminal (CT) domain present in other members of
the CCN family"
/codon_start=1
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WVCDQAVQPAIOPSSAOGHOLSAVDGPECPMNSTWAMGPGSTTCGGLIATRVIS
NMRPCQLEIQRRLRSRCLASRHSWNSAF"
BASE COUNT 375 a 480 c 489 g 395 t
ORIGIN
Query Match 10.6%; Score 80; DB 10; Length 1739;
Best Local Similarity 100.0%; Pred. No. 5.2e-32;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 172 CGAGAGCTGGGGAGATCTCGGACACCTGCATGTCGAGACCCAGGAGGCTGCT 231
DB 413 CGAGAGCTGGGGAGATCTCGGACACCTGCATGTCGAGACCCAGGAGGCTGCT 472
OY 232 TGTGAGCCTGGGGAGGCCC 251
DB 473 TGTGAGCCTGGGGAGGCCC 492
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RESULT 11
AR210337 738 bp DNA linear PAT 20-JUN-2002
LOCUS
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DEFINITION Sequence 38 from patent US 6387657.  
 ACCESSION AR210337  
 VERSION AR210337.1 GI:21512542  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 738)  
 AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.  
 TITLE WISP polypeptides and nucleic acids encoding same  
 JOURNAL Patent: US 6387657-A 38 14-MAY-2002;  
 FEATURES Location/Qualifiers  
 source 1..738  
 /organism="unknown"  
 BASE COUNT 104 a 272 c 238 g 124 t  
 ORIGIN

Query Match 4.2%; Score 32; DB 6; Length 738;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-06;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 GTACCCCTGCTGCTGATGGCTGCTGCTG 158  
 Db 115 GTACCCCTGCTGCTGATGGCTGCTGCTG 146

RESULT 12  
 LOCUS AR210338 841 bp DNA linear PAT 20-JUN-2002  
 DEFINITION Sequence 39 from patent US 6387657.  
 ACCESSION AR210338  
 VERSION AR210338.1 GI:21512543  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 841)  
 AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.  
 TITLE WISP polypeptides and nucleic acids encoding same  
 JOURNAL Patent: US 6387657-A 39 14-MAY-2002;  
 FEATURES Location/Qualifiers  
 source 1..841  
 /organism="unknown"  
 BASE COUNT 124 a 297 c 280 g 140 t  
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 8.4e-06;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 417 GAGGATGTGGCTGCCAGCTGGAGCTGCC 448

RESULT 13  
 LOCUS AX076919 1266 bp DNA linear PAT 22-FEB-2001  
 DEFINITION Sequence 31 from Patent WO0105836.  
 ACCESSION AX076919  
 VERSION AX076919.1 GI:13121575  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens.  
 REFERENCE 1 (bases 1 to 1266)  
 AUTHORS Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and Wood,W.I.  
 TITLE Polypeptide compositions and methods for the treatment of tumors  
 JOURNAL Patent: WO 0105836-A 31 25-JAN-2001;

Genentech, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..1266  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 216 a 418 c 390 g 242 t  
 ORIGIN

Query Match 4.2%; Score 32; DB 6; Length 1266;  
 Best Local Similarity 100.0%; Pred. No. 8e-06;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 GTACCCCTGCTGCTGATGGCTGCTGCTG 158  
 Db 136 GTACCCCTGCTGCTGATGGCTGCTGCTG 167

RESULT 14  
 LOCUS AX464186 1266 bp DNA linear PAT 16-JUL-2002  
 DEFINITION Sequence 319 from Patent WO0140466.  
 ACCESSION AX464186  
 VERSION AX464186.1 GI:21899109  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens.  
 REFERENCE 1 (bases 1 to 1266)  
 AUTHORS Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E., Gao,W.O., Gerritsen,M.E., Goddard,A., Godowski,P.D., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same  
 JOURNAL Patent: WO 0140466-A 319 07-JUN-2001;  
 FEATURES Location/Qualifiers  
 source 1..1266  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 216 a 418 c 390 g 242 t  
 ORIGIN

Query Match 4.2%; Score 32; DB 6; Length 1266;  
 Best Local Similarity 100.0%; Pred. No. 8e-06;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 GTACCCCTGCTGCTGATGGCTGCTGCTG 158  
 Db 136 GTACCCCTGCTGCTGATGGCTGCTGCTG 167

RESULT 15  
 LOCUS AF083500 1283 bp mRNA linear PRI 04-NOV-1998  
 DEFINITION Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds.  
 ACCESSION AF083500  
 VERSION AF083500.1 GI:3462835  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 REFERENCE 1 (bases 1 to 1283)  
 AUTHORS Kumar,S., Hand,A.T., Connor,J.C., Dodds,R.A., Ryan,P.J., Trill,J.G., Fisher,S.M., Stemmion,J.R., Lipschutz,D.B., Bartholomew,V., James,I.E., Rietman,D.J., Gowen,M. and Lee,J.C.  
 TITLE Identification and cloning of CTGF-L from human osteoblasts, a novel cysteine rich protein containing an IGF binding domain  
 JOURNAL Bone 23 (5), S240 (1998)  
 REFERENCE 2 (bases 1 to 1283)

**AUTHORS**  
**TITLE**  
**JOURNAL**

Kumar, S.  
 Direct Submission  
 Submitted (11-AUG-1998) Bone & Cartilage Biology, UW 2109,  
 Smithkline Beecham, 709 Swedeland Road, King of Prussia, PA 19406,  
 USA

**FEATURES**  
**source**

Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /chromosome="20"  
 /map="20q12-q13"  
 /cell\_type="primary osteoblast"

**CDS**

9. .761  
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 factor type C (WVC) and thrombospondin type I (TSP1)  
 domains; member of the CCN (CTGF/cyrl/nov) family; lacks  
 the fourth carboxy-terminal domain present in other  
 members of the CCN family"  
 /codon\_start=1  
 /product="connective tissue growth factor-like protein  
 precursor"  
 /protein\_id="AAC70350.1"  
 /db\_xref="GI:3462836"  
 /translation="MRGTPKTHLAFSLCLLSKVRTQLCPPTCPMPPPRCPLGVP  
 LVLDGCGCCRCVRCARLGEPCDQLHYCDASOGIVCOPGAGPGRGALCLLAEDSSCEV  
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**BASE COUNT** 235 a 418 c 389 g 241 t  
**ORIGIN**

**Query Match**

Best Local Similarity 100.0%; Score 32; DB 9; Length 1283;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 GTACCCCTGTGCTGTGATGGCTGTGCTGCTG 158  
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 Db 135 GTACCCCTGTGCTGTGATGGCTGTGCTGCTG 166

Search completed: July 28, 2003, 21:14:49  
 Job time : 2093.59 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:31:11 ; Search time 197.767 Seconds  
(without alignments)  
8574.520 Million cell updates/sec

Title: US-10-010-408-3

Perfect score: 753  
Sequence: 1 ATGAGGGCAGCCACCTGAT.....CATGGACAGTGTCTTCTAA 753

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 23: /SIDSz/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDSz/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	753	20	AAZ07517
2	753	100.0	1708	20	AAZ07516
3	681	90.4	681	20	AAZ07521
4	210	27.9	210	20	AAZ07519
5	177	23.5	177	20	AAZ07518
6	174	23.1	174	20	AAZ07520
7	90	12.0	753	20	AAZ07518
8	90	12.0	1734	20	AAZ07518
9	32	4.2	199	22	AAZ07518

ALIGNMENTS

10	32	4.2	199	22	ABA38112	Probe #16578 for g
11	32	4.2	199	22	AAK20667	Human brain expres
12	32	4.2	199	22	AAK46811	Human bone marrow
13	32	4.2	199	22	AAI25749	Probe #15682 for g
14	32	4.2	199	22	AAI52650	Probe #21336 used
15	32	4.2	199	22	ABA521124	Human genome-deriv
16	32	4.2	586	22	ABA59703	Human foetal liver
17	32	4.2	586	22	ABA28232	Probe #6698 for ge
18	32	4.2	586	22	AAK07972	Human brain expres
19	32	4.2	586	22	AAK33842	Human bone marrow
20	32	4.2	586	22	AAI16552	Probe #6485 for ge
21	32	4.2	586	22	AAI139568	Probe #8254 used t
22	32	4.2	586	22	ABSO8689	Human genome-deriv
23	32	4.2	738	20	AAZ07501	Human WISP-2 prote
24	32	4.2	750	20	AAZ07487	Human WISP-2 prote
25	32	4.2	841	20	AAZ07502	Human WISP-2 prote
26	32	4.2	1257	20	AAZ07502	Egf-like homologue
27	32	4.2	1266	21	AAA30048	Human PRO261 nucle
28	32	4.2	1266	22	AAZ07502	Human CDNA sequenc
29	32	4.2	1266	22	AAZ07502	PRO261 coding sequ
30	32	4.2	1266	22	AAZ07502	Human angiogenesis
31	32	4.2	1267	21	AAZ07502	Human PRO261 CDNA
32	32	4.2	1285	19	AAV29260	Human connective t
33	32	4.2	1293	20	AAZ07502	Human WISP-2 prote
34	32	4.2	1309	22	AAH28214	Connective tissue
35	32	4.2	1337	22	AAH46952	Human secreted pro
36	32	4.2	1352	22	AAH46952	Human growth facto
37	32	4.2	1522	20	AAI15595	Human full-length
38	32	4.2	2136	22	AAK94706	Human immune/haema
39	32	4.2	13255	22	AAK76842	Human WISP-2 probe
40	27	3.6	51	20	AAZ07502	Human PRO261 hybr
41	27	3.6	51	21	AAZ07502	Probe for PRO261 n
42	27	3.6	51	21	AAZ07502	PRO261 probe #1
43	27	3.6	51	22	AAZ07502	Human PRO261 hybr
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RESULT 1	AAZ07517	standard; cDNA; 753 BP.
ID	AAZ07517	
AC	AAZ07517	
XX		
DT	26-NOV-1999	(first entry)
DE	Rat HICP polypeptide coding sequence.	
XX		
KW	Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;	
KW	cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.	
OS	Rattus sp.	
XX		
PN	W09947556-A2.	
PD	23-SEP-1999.	
XX		
PF	18-MAR-1999;	99WO-US05999.
XX		
PR	19-MAR-1998;	98US-0044273.
XX		
PA	(TUFT ) TUFTS COLLEGE.	
XX		
PI	Castellot JJ;	
XX		
DR	WPI: 1999-562060/47.	
XX	P-PSDB: AAZ27434.	
XX		
PT	Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications	

XX Claim 5; Fig 1; 108bp; English.

CC The invention provides a rat heparin-induced CCN-like protein (HICP)  
 CC protein. Agents that stimulate or inhibit HICP protein activity or  
 CC expression, antisense HICP nucleic acid molecules and HICP antibodies,  
 CC can be used to modulate cell-associated activity. HICP modulators can be  
 CC used to treat disorders characterized by aberrant HICP protein activity  
 CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies  
 CC specific for HICP can be used to detect HICP activity in a biological  
 CC sample. HICP can be used to treat disorders, such as a cardiovascular or  
 CC fibrotic disorder, characterized by aberrant cell proliferation. The  
 CC present sequence represents the coding sequence of rat HICP.

XX Sequence 753 BP; 132 A; 235 C; 230 G; 156 T; 0 other;

Query Match 100.0%; Score 753; DB 20; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGGAGCCCACTGATCCATCTTGGCCACTTCTCTGCTTCTCAATG 60  
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 QY 361 TGCCGCTGTGATGAGCGTGTGCTTCACTGCTGCGCTGTCAGATGAGATGTGGGCTG 420  
 DB 361 TGCCGCTGTGATGAGCGTGTGCTTCACTGCTGCGCTGTCAGATGAGATGTGGGCTG 420  
 QY 421 CCCAGCTGGGACTGCCCCAAGAGATACAGGTGTCAGAGAAAGTGTGCCCCGAG 480  
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 QY 481 TGGGTATGTGACACAGGAGTACACCGGATCCAGCGGTCCACGCGCAAGAACCA 540  
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 QY 541 CTTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
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 QY 601 TGGGGGCCCCCTGTCAACCACTGTGGGTGGGATAGGCAACCGAGTGTCCAAACCA 660  
 DB 601 TGGGGGCCCCCTGTCAACCACTGTGGGTGGGATAGGCAACCGAGTGTCCAAACCA 660  
 QY 661 CGATTCTGCAACTGGAGATCCAAAGCGGCTGTGTGCTGCTGCTGCTGCTGCTGCTG 720  
 DB 661 CGATTCTGCAACTGGAGATCCAAAGCGGCTGTGTGCTGCTGCTGCTGCTGCTGCTG 720  
 QY 721 AGGAGCCACAGCTCATGGAACAGTCTTTCTAA 753  
 DB 721 AGGAGCCACAGCTCATGGAACAGTCTTTCTAA 753

RESULT 2  
 ID AA207516  
 AA207516 standard; cDNA; 1708 BP.

AC AA207516;

DT 26-NOV-1999 (first entry)

DE Rat HICP polypeptide encoding cDNA.

KW Heparin-induced CCN-like protein; HICP; cell-associated activity; as;  
 KM cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.

OS Rattus sp.

PN WO947556-A2.

PD 23-SEP-1999.

PF 18-MAR-1999; 99WO-US05999.

PR 19-MAR-1998; 98US-0044273.

PA (TUFTS ) TUFTS COLLEGE.

PI Castellot JT;

DR WPI; 1999-562060/47.

PT P-PSDB; AAY27434.

PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,  
 used in methods to identify modulators or in diagnostic applications

PS Claim 2; Fig 1; 108bp; English.

CC This cDNA encodes a rat heparin-induced CCN-like protein (HICP) protein.  
 CC Agents that stimulate or inhibit HICP protein activity or expression,  
 CC antisense HICP nucleic acid molecules and HICP antibodies, can be used to  
 CC modulate cell-associated activity. HICP modulators can be used to treat  
 CC disorders characterized by aberrant HICP protein activity or expression.  
 CC Probes capable of hybridizing to HICP mRNA or antibodies specific for  
 CC HICP can be used to detect HICP activity in a biological sample. HICP  
 CC can be used to treat disorders, such as a cardiovascular or fibrotic  
 CC disorder, characterized by aberrant cell proliferation.

Sequence 1708 BP; 362 A; 486 C; 478 G; 382 T; 0 other;

Query Match 100.0%; Score 753; DB 20; Length 1708;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGGAGCCCACTGATCCATCTTGGCCACTTCTCTGCTTCTCAATG 60  
 DB 249 ATGAGGGGAGCCCACTGATCCATCTTGGCCACTTCTCTGCTTCTCAATG 308  
 QY 61 GTGTGTGCCACCTGTGCCGACACCCCTGTACTCTTGGACACACCCCAAGTCCCA 120  
 DB 309 GTGTGTGCCACCTGTGCCGACACCCCTGTACTCTTGGACACACCCCAAGTCCCA 368  
 QY 121 CAGGGGGTACCCCTGGTGTGATGGCTGTGCTGCTGTAAGTGTGTGACAGAGGCTG 180  
 DB 369 CAGGGGGTACCCCTGGTGTGATGGCTGTGCTGCTGTAAGTGTGTGACAGAGGCTG 428  
 QY 181 GGGGAGTCTCTGGACACCTGATGTGCGACCCACGAGGAGGCTGTGTGACGCT 240  
 DB 429 GGGGAGTCTCTGGACACCTGATGTGCGACCCACGAGGAGGCTGTGTGACGCT 488  
 QY 241 GGGGAGGAGCCCTGGGCGCCATGGGCTGTGTCTCTTGGATGAGATACGCTAGCT 300  
 DB 489 GGGGAGGAGCCCTGGGCGCCATGGGCTGTGTCTCTTGGATGAGATACGCTAGCT 548  
 QY 301 GAGGTGAATGGCCGAGGATGATGAGAGACCTTAAACCAATGACAGGGTCTG 360  
 DB 548 GAGGTGAATGGCCGAGGATGATGAGAGACCTTAAACCAATGACAGGGTCTG 360



XX	OS	Rattus sp.	XX
XX	PN	MO9947556-A2.	XX
XX	PD	23-SEP-1999.	XX
XX	PF	18-MAR-1999;	XX
XX	PR	99MO-US05999.	XX
XX	PI	19-MAR-1998;	XX
XX	PA	98US-0044273.	XX
XX	PI	(TUFTS COLLEGE.	XX
XX	PI	Castellot JJ;	XX
XX	DR	WPI: 1999-562060/47.	XX
XX	DR	P-PSDB: AAY27438.	XX
XX	PT	Nucleic acid sequences encoding rat heparin-induced CCN-like protein,	XX
XX	PS	used in methods to identify modulators or in diagnostic applications	XX
XX	PS	Disclosure: Page 104; 108pp; English.	XX
CC	CC	The invention provides a rat heparin-induced CCN-like protein (HICP)	CC
CC	CC	protein. Agents that stimulate or inhibit HICP protein activity or	CC
CC	CC	expression, antisense HICP nucleic acid molecules and HICP antibodies,	CC
CC	CC	can be used to modulate cell-associated activity. HICP modulators can be	CC
CC	CC	used to treat disorders characterized by aberrant HICP protein activity	CC
CC	CC	or expression. Probes capable of hybridizing to HICP mRNA or antibodies	CC
CC	CC	specific for HICP can be used to detect HICP activity in a biological	CC
CC	CC	sample. HICP can be used to treat disorders, such as cardiovascular or	CC
CC	CC	fibrotic disorder, characterized by aberrant cell proliferation. The	CC
CC	CC	present sequence represents a nucleotide sequence encoding the insulin-	CC
XX	XX	like growth factor binding protein (IGFBP) domain of HICP polypeptide.	XX
SO	SO	Sequence 210 BP; 27 A; 65 C; 74 G; 44 T; 0 other;	SO
Query Match	27.98;	Score 210; DB 20; Length 210;	
Best Local Similarity	100.0%;	Pred. No. 2.1e-89;	
Matches 210;	Conservative 0;	Mismatches 0; Indels 0	
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OY	OY	130 CCCCTGTGTGTGATGCGTGTGGTGTGCTGTAAGTGTGTGACGAGGCTGGGGAGTCC 189	OY
Db	Db	61 CCCCTGTGTGTGATGCGTGTGGTGTGCTGTAAGTGTGTGACGAGGCTGGGGAGTCC 120	Db
OY	OY	190 TGGACACACCGCATGTCTGTGGACCCGACGAGGGCGTTTGCACCTGGGGCAGGC 249	OY
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OY	OY	250 CCTGGCGGCCATGGGGCTGTGTCTCTTTG 279	OY
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AAZ07518			
AAZ07518		standard; cDNA; 177 BP.	
AAZ07518:			
AC	AC	26-NOV-1999 (first entry)	AC
XX	XX		XX
DE	DE	Rat HICP VMC domain encoding cDNA.	DE
XX	XX		XX
KM	KM	Heparin-induced CCN-like protein; HICP: cell-associated activity; ss:	KM
KM	KM	cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;	KM
XX	XX	von Willebrand C domain; VMC.	XX
XX	XX	Rattus sp.	XX

	XX	MW994756-AZ.	
	PX		
	PD	23-SEP-1999.	
	PF		
	PI	18-MAR-1999;	99WO-US05999.
	PR	19-MAR-1998;	98US-0044273.
	PA	(TUFTS ) TUFTS COLLEGE.	
	PT	Castellot JJ:	
	DR	WPJ: 1999-562060/47.	
	XN	P-FSDb; AAAY27436.	
	XT	Nucleic acid sequences encoding rat heparin-induced CCN-like protein,	-
	PS	used in methods to identify modulators or in diagnostic applications -	
	CC	Disclosure: Page 103; 108pp; English.	
	CC	The invention provides a rat heparin-induced CCN-like protein (HICP)	
	CC	protein. Agents that stimulate or inhibit HICP protein activity or	
	CC	expression, antisense HICP nucleic acid molecules and HICP antibodies,	
	CC	can be used to modulate cell-associated activity. HICP modulators can be	
	CC	used to treat disorders characterized by aberrant HICP protein activity	
	CC	or expression. Probes capable of hybridizing to HICP mRNA or antibodies	
	CC	specific for HICP can be used to detect HICP activity in a biological	
	CC	sample. HICP can be used to treat disorders, such as a cardiovascular or	
	CC	fibrotic disorder, characterized by aberrant cell proliferation. The	
	SQ	present sequence represents a cDNA encoding the von Willebrand C (VWC)	
	XX	a domain of the HICP polypeptide.	
	XX	Sequence 177 BP; 35 A; 47 C; 60 G; 35 T; 0 other;	
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Dd	Bd	Best Local Similarity	100.0%; Pred. No. 8.8e-74;
		Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
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		TT	
Dd		1 TGTGAGTGTAATGGCGCGAAGTAGCTGATGAGAAGACCTTAAACCATAATTCAGAGGC	60
Oy		358 CTGTGCCGCTGTATGACGTGTGCTTCACTGCTGCCGCGTGTGCAAGTGAAGATGTGCG	417
		TT	
Dd		61 CTGTGCCGCTGTGTGAGAGGTGTGCTTCACTGCTGCCGCGTGTGCAAGTGAAGATGTGCG	120
Oy		418 CTGCCCAAGCTGTGGAGCTGCCAGCGCCCCCAAGAAGATACAGGTGCCAGAAAAGTGTGC	474
		TT	
Dd		121 CTGCCCAAGCTGTGGAGCTGCCAGCGCCCCCAAGAAGATACAGGTGCCAGAAAAGTGTGC	177
		TT	
		RESULT 6	
	AAs07520		
	AD D	AAc07520 standard; CDNA: 174 BP.	
xx	Ac	AAz07520;	
xn	Ad		
xr	AE	26-NOV-1999 (first entry)	
xs	AF		
xt	Ag	Rat HICP TSPl domain encoding CDNA.	
xy	AI	Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;	
yx	KM	cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;	
yy	KL	Thrombospondin 1 domain; TSPl.	
yx	OS		
ys	Rattus sp.		
yt	Wo994756-A2.		
yz	PX		
zx	PN	23-SEP-1999.	
zy	PD		
zz	Tf	18-MAR-1999;	99WO-US05999.



XX 19-MAR-1998; 98US-0044273.  
 XX (TUFT ) TUFTS COLLEGE.  
 PA Castellet JJ;  
 XX WPI: 1999-562060/47.  
 DR P-PSDB; AAY27439.  
 XX  
 PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,  
 XX used in methods to identify modulators or in diagnostic applications  
 XX  
 PS Disclosure; Page 105; 108pp; English.  
 XX  
 CC The invention provides a rat heparin-induced CCN-like protein (HICP)  
 CC protein. Agents that stimulate or inhibit HICP protein activity or  
 CC expression, antisense HICP nucleic acid molecules and HICP antibodies,  
 CC can be used to modulate cell-associated activity. HICP modulators can be  
 CC used to treat disorders characterized by aberrant HICP protein activity  
 CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies  
 CC specific for HICP can be used to detect HICP activity in a biological  
 CC sample. HICP can be used to treat disorders, such as a cardiovascular or  
 CC fibrotic disorder, characterized by aberrant cell proliferation. The  
 CC present sequence represents a nucleotide sequence encoding the  
 CC thrombospondin 1 (TSP1) domain of the HICP polypeptide.  
 XX  
 SQ Sequence 174 BP; 36 A; 62 C; 45 G; 31 T; 0 other;

Query Match 23.1%; Score 174; DB 20; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-72;  
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 577 CCTGTCCAAATTGAGACAGCCTGGGCCCCCTGTCACACCTGTGGGCTGGGATA 636  
 DB 1 CTTTGTCCAAATTGAGACAGCCTGGGCCCCCTGTCACACCTGTGGGCTGGGATA 60  
 OY 637 GCCACCCGAGTGTCCACACGACGATTCCTCCACTGAGATCCAAAGCCGCTGTGT 696  
 DB 61 GCCACCCGAGTGTCCACACGACGATTCCTCCACTGAGATCCAAAGCCGCTGTGT 120  
 OY 697 CTGCCAGAGCCCTCTGGCAGCCAGGACGACGATTCGATGGAACAGTCTTTC 750  
 DB 121 CTGCCAGAGCCCTCTGGCAGCCAGGACGACGATTCGATGGAACAGTCTTTC 174

RESULT 7  
 AAX76489/C  
 ID AAX76489 standard; DNA; 753 BP.

XX AAX76489;  
 XX  
 DT 06-AUG-1999 (first entry)  
 DE Mouse WISP-2 protein complementary nucleotide sequence SEQ ID NO:18.  
 XX  
 KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;  
 KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;  
 KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;  
 KW tissue growth disorder; skin disorder; desmoplasia; fibrotic lesion;  
 KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;  
 KW connective tissue disorder; catabolic state; inflammation;  
 KW testicular-related disorder; angiogenesis; immunological disorder; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN W09921998-A1.  
 XX  
 PD 06-MAY-1999.  
 XX  
 PF 29-OCT-1998; 98WO-US22991.  
 XX  
 PR 14-APR-1998; 98US-0081695.

PR 29-OCT-1997; 97US-0063704.  
 PR 03-FEB-1998; 98US-0073612.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;  
 PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;  
 XX WPI: 1999-337420/28.  
 DR  
 XX  
 PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3  
 XX  
 PS Disclosure; Page 179-180; 284pp; English.  
 XX  
 CC The present invention describes Wnt-1 induced secreted polypeptides,  
 CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2  
 CC and WISP-3 have homology to connective tissue growth factor (CTGF).  
 CC products from the present invention can be used to treat WISP-related  
 CC disorders such as breast, ovarian, and colon cancer or melanoma. The  
 CC products can be used to treat arteriosclerosis. The products can also be  
 CC used to treat other diseases e.g. benign and malignant tumours,  
 CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,  
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and  
 CC blastocoeleic disorders, haematopoiesis-related disorders, tissue-growth  
 CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney  
 CC disorders, bone-related disorders such as osteoporosis, trauma such as  
 CC burns, incisions, and other wounds, connective tissue disorders,  
 CC catabolic states, testicular-related disorders, and inflammation,  
 CC angiogenic and immunologic disorders including arteriosclerosis. The  
 CC products can also be used for detection and diagnosis especially of  
 CC individuals with neoplastic cell growth or proliferation. The products  
 CC can be used in the production of transgenic or knock-out animals.  
 CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing  
 CC cells.  
 XX  
 SQ Sequence 753 BP; 159 A; 229 C; 238 G; 127 T; 0 other;

Query Match 12.0%; Score 90; DB 20; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-32;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 162 AGTGTGACGAGAGGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCA 221  
 DB 592 AGTGTGACGAGAGGCTGGGGAGTCTCTGGACACCTGCATGTCTGGACCCAGCA 533  
 OY 222 GGGCTGTGTGTGACGCTGGGGAGGCC 251  
 DB 532 GGGCTGTGTGTGACGCTGGGGAGGCC 503

RESULT 8  
 AAX76488  
 ID AAX76488 standard; DNA; 1734 BP.

XX AAX76488;  
 XX  
 DT 06-AUG-1999 (first entry)  
 DE Mouse WISP-2 protein nucleotide sequence SEQ ID NO:17.  
 XX  
 KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;  
 KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;  
 KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;  
 KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;  
 KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;  
 KW connective tissue disorder; catabolic state; inflammation;  
 KW testicular-related disorder; angiogenesis; immunological disorder; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN W09921998-A1.  
 XX  
 PD 06-MAY-1999.

```

XX 29-OCT-1998; 98WO-US22991.
PF 14-APR-1998; 98US-0081695.
XX 29-OCT-1997; 98US-0063704.
PR 03-FEB-1998; 98US-0073612.
XX (GETH ) GENENTECH INC.
XX Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX WPI; 1999-337420/28.
DR P-PSDB; AAY17651.
XX
XX New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
PT Example 2; Page 178-179; 284pp; English.
XX
XX The present invention describes Wnt-1 induced secreted polypeptides,
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
CC and WISP-3 have homology to connective tissue growth factor (CTGF).
CC Products from the present invention can be used to treat WISP-related
CC disorders such as breast, ovarian, and colon cancer or melanoma. The
CC products can be used to treat arteriosclerosis. The products can also be
CC used to treat other diseases e.g. benign and malignant tumours,
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and
CC blastocoele disorders, haematopoiesis-related disorders, tissue-growth
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
CC disorders, bone-related disorders such as osteoporosis, trauma such as
CC burns, incisions, and other wounds, connective tissue disorders,
CC catabolic states, testicular-related disorders, and inflammatory,
CC angiogenic and immunologic disorders including arteriosclerosis. The
CC products can also be used for detection and diagnosis especially of
CC individuals with neoplastic cell growth or proliferation. The products
CC can be used in the production of transgenic or knock-out animals.
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
CC cells.
XX
XX Sequence 1734 BP; 355 A; 491 C; 495 G; 393 T; 0 other:
SQ
XX
XX Query Match 12.0%; Score 90; DB 20; Length 1734;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-32;
XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 162 AGTGTGTGACGAGAGGCTGGGGAGTCTGCGACACCTGATGTCTGCGACCCAGCCA 221
DB 418 AGTGTGTGACGAGAGGCTGGGGAGTCTGCGACACCTGATGTCTGCGACCCAGCCA 477
XX
XX 222 GGGCCTGTTTGTACGCTGGGGCAGGCC 251
DB 478 GGGCCTGTTTGTACGCTGGGGCAGGCC 507
XX
XX
XX RESULT 9
XX ABA72245
XX ID ABA72245 standard; DNA; 199 BP.
XX
XX ABA72245;
XX
XX 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #20550.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
XX Homo sapiens.
XX
XX WO200157277-A2.
XX
XX 09-AUG-2001.
XX

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PF 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 4; SEQ ID NO 20550; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
SQ
XX
XX Query Match 4.2%; Score 32; DB 22; Length 199;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-05;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 406 GAGATGTGCGGCTGCCAGCTGGGACTGCCC 437
DB 129 GAGATGTGCGGCTGCCAGCTGGGACTGCCC 160
XX
XX
XX RESULT 10
XX ABA38112
XX ID ABA38112 standard; DNA; 199 BP.
XX
XX ABA38112;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #16578 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX

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```

QY 406 GAGGATGTGCGGCTGCCAGCTGGGACTGCC 437
DB 129 GAGGATGTGCGGCTGCCAGCTGGGACTGCC 160

RESULT 13
AA125749
ID AA125749 standard; DNA; 199 BP.
AC AA125749;
XX
XX 12-OCT-2001 (first entry)
DE Probe #15682 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 25; SEQ ID No 15682; 487bp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
SQ

Query Match 4.2%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX 17-OCT-2001 (first entry)
DT
XX
XX Probe #21336 used to measure gene expression in human placenta sample.
DE
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID No 21336; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
SQ

Query Match 4.2%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX WO200186003-A2.  
 XX 15-NOV-2001.  
 XX 30-JAN-2001; 2001WO-US00665.  
 XX 04-FEB-2000; 2000US-180312P.  
 XX 26-MAY-2000; 2000US-207456P.  
 XX 30-JUN-2000; 2000US-0608408.  
 XX 03-AUG-2000; 2000US-0632366.  
 XX 21-SEP-2000; 2000US-234687P.  
 XX 27-SEP-2000; 2000US-236359P.  
 XX 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2002-114183/15.  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples -  
 PS Claim 4; SEQ ID No 21115; 634pp; English.  
 XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Kartagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a single exon  
 CC probe open reading frame of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

QY 406 GAGGATGTGGGGCTGCCAGCTGGGACTGCC 437  
 Db 129 GAGGATGTGGGGCTGCCAGCTGGGACTGCC 160

Search completed: July 28, 2003, 15:55:00  
 Job time : 198.767 secs

Query Match 4.2%; Score 32; DB 24; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:50:06 ; Search time 41.1485 Seconds  
(without alignments)  
5612.050 Million cell updates/sec

Title: US-10-010-408-3  
Perfect score: 753  
Sequence: 1 ATGAGGGGACAGCCACTGAT.....CATGAACAGTCTTCTAA 753

Scoring table: OLIGO\_NMC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_NM: \*  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	12.0	1734	4	US-09-182-145-17 Sequence 17, Appl
2	90	12.0	1734	4	US-09-182-145-18 Sequence 18, Appl
3	32	4.2	738	4	US-09-182-145-38 Sequence 38, Appl
4	32	4.2	841	4	US-09-182-145-39 Sequence 39, Appl
5	32	4.2	1293	4	US-09-182-145-13 Sequence 13, Appl
6	32	4.2	1293	4	US-09-182-145-14 Sequence 14, Appl
7	27	3.6	51	4	US-09-182-145-117 Sequence 117, App
8	19	2.5	616	4	US-09-385-982-220 Sequence 220, App
9	19	2.5	1196	4	US-09-149-476-57 Sequence 225, App
10	19	2.5	1220	4	US-09-149-476-57 Sequence 225, App
11	19	2.5	1514	2	US-09-213-768-1 Sequence 1, Appl
12	19	2.5	1539	2	US-09-668-680-13 Sequence 13, Appl
13	18	2.4	20	2	US-09-213-768-2 Sequence 2, Appl
14	18	2.4	3727	1	US-08-249-380-1 Sequence 1, Appl
15	18	2.3	44	4	US-09-182-145-152 Sequence 152, App
16	17	2.3	464	3	US-08-691-814B-117 Sequence 117, App
17	17	2.3	480	3	US-09-188-930-206 Sequence 206, App
18	17	2.3	482	4	US-08-691-814B-120 Sequence 120, App
19	17	2.3	614	4	US-08-998-416-151 Sequence 151, App
20	17	2.3	896	3	US-09-188-930-36 Sequence 36, Appl
21	17	2.3	933	3	US-08-987-743-1 Sequence 1, Appl
22	17	2.3	1308	3	US-08-987-743-5 Sequence 5, Appl
23	17	2.3	1743	3	US-08-665-259-20 Sequence 20, Appl
24	17	2.3	1743	3	US-08-762-500-20 Sequence 20, Appl
25	17	2.3	1821	3	US-09-149-476-90 Sequence 90, Appl
26	17	2.3	1974	3	US-08-762-500-78 Sequence 78, Appl
27	17	2.3	2329	1	US-08-455-559-9 Sequence 9, Appl

C 28	17	2.3	2329	4	US-09-145-060-9	Sequence 9, Appl
C 29	17	2.3	2329	5	PCT-US94-00657-9	Sequence 9, Appl
C 30	17	2.3	2517	3	US-08-733-360A-4	Sequence 4, Appl
C 31	17	2.3	2517	3	US-08-987-743-16	Sequence 16, Appl
C 32	17	2.3	2517	4	US-08-916-935-4	Sequence 4, Appl
C 33	17	2.3	3865	4	US-09-149-476-296	Sequence 296, App
C 34	17	2.3	6803	3	US-08-665-259-19	Sequence 19, Appl
C 35	17	2.3	6803	3	US-08-762-500-19	Sequence 19, Appl
C 36	17	2.3	7874	4	US-09-780-175-96	Sequence 96, Appl
C 37	17	2.3	81001	4	US-09-750-580-1	Sequence 1, Appl
C 38	16	2.1	21	4	US-08-477-928A-27	Sequence 27, Appl
C 39	16	2.1	31	1	US-08-524-757-34	Sequence 34, Appl
C 40	16	2.1	366	4	US-09-660-552-30	Sequence 30, Appl
C 41	16	2.1	424	4	US-09-280-116-206	Sequence 206, App
C 42	16	2.1	435	4	US-09-397-787-280	Sequence 280, App
C 43	16	2.1	441	4	US-09-660-552-28	Sequence 28, Appl
C 44	16	2.1	465	4	US-09-149-476-12	Sequence 12, Appl
C 45	16	2.1	524	4	US-09-149-476-199	Sequence 199, App

#### ALIGNMENTS

```
RESULT 1
US-09-182-145-17
: Sequence 17, Application US/09182145B
: Patent No. 6387657
:
: GENERAL INFORMATION:
: APPLICANT: Bolstein, David A.
: APPLICANT: Cohen, Robert
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Audrey L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Lawrence, David A.
: APPLICANT: Levine, Arnold J.
: APPLICANT: Pennica, Diane
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: P1176R2
: CURRENT APPLICATION NUMBER: US/09/182,145B
: EARLIER FILING DATE: 1998-10-29
: EARLIER APPLICATION NUMBER: US 60/063,704
: EARLIER FILING DATE: 1997-10-29
: EARLIER APPLICATION NUMBER: US 60/073,612
: EARLIER FILING DATE: 1998-02-04
: EARLIER APPLICATION NUMBER: US 60/081,695
: EARLIER FILING DATE: 1998-04-14
: NUMBER OF SEQ ID NOS: 156
: SEQ ID NO 17
: LENGTH: 1734
: TYPE: DNA
: ORGANISM: Mus musculus
: US-09-182-145-17

Query Match          12.0%: Score 90; DB 4; Length 1734;
Best Local Similarity 100.0%: Pred. No. 6.8e-34;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 162 AGTGTGACGAGGAGGCTGGGGAGTCTCGAGACCACTGATGTGACCCACCA 221
DB 418 AGTGTGACGAGGAGGCTGGGGAGTCTCGAGACCACTGATGTGACCCACCA 477
OY 222 GGGCTGTGTTGTGACCTGGGCGAGGCC 251
DB 478 GGGCTGTGTTGTGACCTGGGCGAGGCC 507

RESULT 2
US-09-182-145-18/C
: Sequence 18, Application US/09182145B
: Patent No. 6387657
: GENERAL INFORMATION:
```

```

: APPLICANT: Botstein, David A.
: APPLICANT: Cohen, Robert
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Lawrence, David A.
: APPLICANT: Levine, Arnold J.
: APPLICANT: Pennica, Diane
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: P1176R2
: CURRENT APPLICATION NUMBER: US/09/182,145B
: CURRENT FILING DATE: 1998-10-29
: EARLIER APPLICATION NUMBER: US 60/063,704
: EARLIER FILING DATE: 1997-10-29
: EARLIER APPLICATION NUMBER: US 60/073,612
: EARLIER FILING DATE: 1998-02-04
: EARLIER APPLICATION NUMBER: US 60/081,695
: EARLIER FILING DATE: 1998-04-14
: NUMBER OF SEQ ID NOS: 156
: SEQ ID NO 18
: LENGTH: 1734
: TYPE: DNA
: ORGANISM: Mus musculus
: US-09-182-145-18

Query Match          12.0%; Score 90; DB 4; Length 1734;
Best Local Similarity 100.0%; Pred. No. 6,8e-34;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 AGTGTGTGACGAGCGAGCTGGGGAGCTCTGCGACCACTGCATGTCTGCGACCCAGCCA 221
DB 1317 AGTGTGTGACGAGCGAGCTGGGGAGCTCTGCGACCACTGCATGTCTGCGACCCAGCCA 1258
QY 222 GGGCCTGGTTGTGTCAGCCTGGGGGAGGCC 251
DB 1257 GGGCCTGGTTGTGTCAGCCTGGGGGAGGCC 1228

RESULT 3
US-09-182-145-38
: Sequence 38, Application US/09182145B
: Patent No. 6387657
: GENERAL INFORMATION:
: APPLICANT: Botstein, David A.
: APPLICANT: Cohen, Robert
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Lawrence, David A.
: APPLICANT: Levine, Arnold J.
: APPLICANT: Pennica, Diane
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: P1176R2
: CURRENT APPLICATION NUMBER: US/09/182,145B
: CURRENT FILING DATE: 1998-10-29
: EARLIER APPLICATION NUMBER: US 60/063,704
: EARLIER FILING DATE: 1997-10-29
: EARLIER APPLICATION NUMBER: US 60/073,612
: EARLIER FILING DATE: 1998-02-04
: EARLIER APPLICATION NUMBER: US 60/081,695
: EARLIER FILING DATE: 1998-04-14
: NUMBER OF SEQ ID NOS: 156
: SEQ ID NO 38
: LENGTH: 738
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-182-145-38

Query Match          4.2%; Score 32; DB 4; Length 738;
```

```

: APPLICANT: Botstein, David A.
: APPLICANT: Cohen, Robert
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Lawrence, David A.
: APPLICANT: Levine, Arnold J.
: APPLICANT: Pennica, Diane
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: P1176R2
: CURRENT APPLICATION NUMBER: US/09/182,145B
: CURRENT FILING DATE: 1998-10-29

Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGATGATGCTGTGCTGCTG 158
DB 115 GTACCCCTGCTGATGATGCTGTGCTGCTG 146

RESULT 4
US-09-182-145-39
: Sequence 39, Application US/09182145B
: Patent No. 6387657
: GENERAL INFORMATION:
: APPLICANT: Botstein, David A.
: APPLICANT: Cohen, Robert
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Lawrence, David A.
: APPLICANT: Levine, Arnold J.
: APPLICANT: Pennica, Diane
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: P1176R2
: CURRENT APPLICATION NUMBER: US/09/182,145B
: CURRENT FILING DATE: 1998-10-29
: EARLIER APPLICATION NUMBER: US 60/063,704
: EARLIER FILING DATE: 1997-10-29
: EARLIER APPLICATION NUMBER: US 60/073,612
: EARLIER FILING DATE: 1998-02-04
: EARLIER APPLICATION NUMBER: US 60/081,695
: EARLIER FILING DATE: 1998-04-14
: NUMBER OF SEQ ID NOS: 156
: SEQ ID NO 39
: LENGTH: 841
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1-841
: OTHER INFORMATION: Sequence is synthesized.
: Patent No. 6387657
: US-09-182-145-39

Query Match          4.2%; Score 32; DB 4; Length 841;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 GAGATGTGCGGCTGCCAGCTGGGACTGCC 437
DB 417 GAGATGTGCGGCTGCCAGCTGGGACTGCC 448

RESULT 5
US-09-182-145-13
: Sequence 13, Application US/09182145B
: Patent No. 6387657
: GENERAL INFORMATION:
: APPLICANT: Botstein, David A.
: APPLICANT: Cohen, Robert
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Lawrence, David A.
: APPLICANT: Levine, Arnold J.
: APPLICANT: Pennica, Diane
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: P1176R2
: CURRENT APPLICATION NUMBER: US/09/182,145B
: CURRENT FILING DATE: 1998-10-29
```



EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 13  
LENGTH: 1293  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-182-145-13

Query Match 4.2%; Score 32; DB 4; Length 1293;  
Best Local Similarity 100.0%; Pred. No. 3.7e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTGTGATGGCTGTGCTGCTG 158  
DB 148 GTACCCCTGGTGTGATGGCTGTGCTGCTG 179

RESULT 6  
US-09-182-145-14/c  
Sequence 14, Application US/09182145B  
Patent No. 6387657  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 14  
LENGTH: 1293  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-182-145-14

Query Match 4.2%; Score 32; DB 4; Length 1293;  
Best Local Similarity 100.0%; Pred. No. 3.7e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTGTGATGGCTGTGCTGCTG 158  
DB 1146 GTACCCCTGGTGTGATGGCTGTGCTGCTG 1115

RESULT 7  
US-09-182-145-117  
Sequence 117, Application US/09182145B  
Patent No. 6387657  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.

APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 117  
LENGTH: 51  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1-51  
OTHER INFORMATION: Sequence is synthesized.  
Patent No. 6387657  
US-09-182-145-117

Query Match 3.6%; Score 27; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.00093;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 CCTGGTGTGATGGCTGTGCTGCTGCTG 158  
DB 1 CCTGGTGTGATGGCTGTGCTGCTGCTG 27

RESULT 8  
US-09-385-982-220/c  
Sequence 220, Application US/09385982  
Patent No. 6262334  
GENERAL INFORMATION:  
APPLICANT: ENDEGE, WILSON O., ET AL.  
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
FILE REFERENCE: CCDNA-260XX  
CURRENT APPLICATION NUMBER: US/09/385,982  
CURRENT FILING DATE: 1999-08-30  
EARLIER APPLICATION NUMBER: 09/328,111  
EARLIER FILING DATE: 1999-06-08  
EARLIER APPLICATION NUMBER: 60/7117,393  
EARLIER FILING DATE: 1999-01-27  
EARLIER APPLICATION NUMBER: 60/098,639  
EARLIER FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 544  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 220  
LENGTH: 616  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(616)  
OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-220

Query Match 2.5%; Score 19; DB 4; Length 616;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TGATGACGTGGCTTACAC 387  
DB 127 TGATGACGTGGCTTACAC 109

RESULT 9  
US-09-149-476-225/c  
Sequence 225, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002p1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595

EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 2.58; Score 19; DB 4; Length 1196;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0;  
Indels 0; Gaps 0;

OY 369 TGATGAGCGTGGCTTACC 387  
|||||  
Db 134 TGATGAGCGTGGCTTACC 116

RESULT 10  
US-09-149-476-57/C  
Sequence 57, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002p1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
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EARLIER APPLICATION NUMBER: 60/047,592  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
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EARLIER APPLICATION NUMBER: 60/043,311

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EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
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EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
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EARLIER FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/047,594  
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EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
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EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

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Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TGATGACGTGCTTCACC 387  
DB 128 TGATGACGTGCTTCACC 110

RESULT 11  
US-09-213-768-1/c  
Sequence 1, Application US/09213768  
Patent No. 5985664  
GENERAL INFORMATION:  
APPLICANT: Brenda F. Baker  
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION  
FILE REFERENCE: RTS-0026  
CURRENT APPLICATION NUMBER: US/09/213,768  
CURRENT FILING DATE: 1998-12-17  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 1

LENGTH: 1514  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (136)..(441)  
US-09-213-768-1

Query Match 2.5%; Score 19; DB 2; Length 1514;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TGATGACGGTGGCTTCAC 387  
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Db 136 TGATGACGGTGGCTTCAC 118

RESULT 12  
US-09-668-680-13  
Sequence 13, Application US/09668680  
Patent No. 6436703  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Zhou, Ping  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aildong J.  
APPLICANT: Xu, Chongjun  
APPLICANT: Dimanac, Radoje T.  
TITLE OF INVENTION: No. 6436703el Nucleic Acids and  
FILE REFERENCE: 790CIP2A  
CURRENT APPLICATION NUMBER: US/09/668, 680  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: pl\_genes Version 2.0  
SEQ ID NO 13  
LENGTH: 1539  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (130)..(1539)  
US-09-668-680-13

Query Match 2.5%; Score 19; DB 4; Length 1539;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CTTCCTGCTCTCTCA 57  
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Db 774 CTTCCTGCTCTCTCA 792

RESULT 13  
US-09-213-768-2/c  
Sequence 2, Application US/09213768  
Patent No. 5985664  
GENERAL INFORMATION:  
APPLICANT: Brenda F. Baker  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRY EXPRESSION  
FILE REFERENCE: RFS-0026  
CURRENT APPLICATION NUMBER: US/09/213,768  
CURRENT FILING DATE: 1998-12-17  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 2

LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR Primer  
US-09-213-768-2

Query Match 2.4%; Score 18; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TGATGACGGTGGCTTCAC 386  
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Db 18 TGATGACGGTGGCTTCAC 1

RESULT 14  
US-08-249-380-1/c  
Sequence 1, Application US/08249380  
Patent No. 5827685  
GENERAL INFORMATION:  
APPLICANT: Lindquist, Susan  
TITLE OF INVENTION: Methods and Compositions of Genetic  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,380  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/710,187  
FILING DATE: 31-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD:024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3727 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-249-380-1

Query Match 2.4%; Score 18; DB 1; Length 3727;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACTGATCATCTCTGGC 32  
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Db 1143 ACTGATCATCTCTGGC 1126

RESULT 15  
US-09-182-145-152/c  
Sequence 152, Application US/09182145B  
Patent No. 6387657

GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: MISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT APPLICATION NUMBER: US/09/182,145B  
CURRENT FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: US 60/063,704  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: US 60/073,612  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: US 60/081,695  
EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 152  
LENGTH: 44  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1-44  
OTHER INFORMATION: Sequence is synthesized.  
Patent No. 6387657  
US-09-182-145-152

Query Match 2.3%; Score 17; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 ACACCAACCCCACTGCC 119  
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DB 44 ACACCAACCCCACTGCC 28

Search completed: July 28, 2003, 15:58:56  
Job time : 42.1485 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:30:21 ; Search time 185.44 Seconds  
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8377.033 Million cell updates/sec

Title: US-10-010-408-3

Perfect score: 753  
Sequence: 1 ATGAGGGGACCCACCTGAT.....CATGACAGCTTTCTTAA 753

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1439767 seqs, 1031500376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PC1\_NEW\_PUB.seq:\*
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- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	753	100.0	1708	US-10-010-408-1	Sequence 1, Appli
3	681	90.4	681	US-10-010-408-12	Sequence 12, Appli
4	210	27.9	210	US-10-010-408-8	Sequence 8, Appli
5	177	23.5	177	US-10-010-408-5	Sequence 5, Appli
6	174	23.1	174	US-10-010-408-10	Sequence 10, Appli
7	90	12.0	1734	US-10-112-267-17	Sequence 17, Appli
8	90	12.0	1734	US-10-112-267-18	Sequence 18, Appli
9	32	4.2	199	US-09-864-761-33432	Sequence 23432, A
10	32	4.2	586	US-09-864-761-6698	Sequence 6698, Ap
11	32	4.2	738	US-10-112-267-38	Sequence 38, Appli
12	32	4.2	841	US-10-112-267-39	Sequence 39, Appli
13	32	4.2	1266	US-10-137-866-319	Sequence 319, App
14	32	4.2	1266	US-10-146-726-319	Sequence 319, App
15	32	4.2	1266	US-10-146-727-319	Sequence 319, App
16	32	4.2	1266	US-10-146-788-319	Sequence 319, App

17	32	4.2	1266	14	US-10-152-380-319	Sequence 319, App
18	32	4.2	1266	15	US-10-153-934-319	Sequence 319, App
19	32	4.2	1266	15	US-10-028-072-319	Sequence 319, App
20	32	4.2	1266	15	US-10-121-049-319	Sequence 319, App
21	32	4.2	1266	15	US-10-123-904-319	Sequence 319, App
22	32	4.2	1266	15	US-10-140-470-319	Sequence 319, App
23	32	4.2	1266	15	US-10-175-746-319	Sequence 319, App
24	32	4.2	1266	15	US-10-176-918-319	Sequence 319, App
25	32	4.2	1266	15	US-10-176-921-319	Sequence 319, App
26	32	4.2	1266	15	US-10-137-865-319	Sequence 319, App
27	32	4.2	1266	15	US-10-140-474-319	Sequence 319, App
28	32	4.2	1266	15	US-10-142-431-319	Sequence 319, App
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32	32	4.2	1266	15	US-10-123-262-319	Sequence 319, App
33	32	4.2	1266	15	US-10-142-423-319	Sequence 319, App
34	32	4.2	1266	15	US-10-121-050-319	Sequence 319, App
35	32	4.2	1266	15	US-10-141-755-319	Sequence 319, App
36	32	4.2	1266	15	US-10-143-032-319	Sequence 319, App
37	32	4.2	1266	15	US-10-123-108-319	Sequence 319, App
38	32	4.2	1266	15	US-10-123-236-319	Sequence 319, App
39	32	4.2	1266	15	US-10-123-261-319	Sequence 319, App
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42	32	4.2	1266	15	US-10-121-045-319	Sequence 319, App
43	32	4.2	1266	15	US-10-123-292-319	Sequence 319, App
44	32	4.2	1266	15	US-10-123-603-319	Sequence 319, App
45	32	4.2	1266	15	US-10-124-819-319	Sequence 319, App

## ALIGNMENTS

RESULT 1  
US-10-010-408-3  
Sequence 3, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castelliott, Jr.  
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules  
and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <unknown>  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 753 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..750  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-10-010-408-3

Query Match 100.0%; Score 753; DB 15; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CAGGGGGATACCCCTGGTGTGATGGCTGTGCTGTCTTGAAGTGTGTGACGAGAGCTG 180
OY 181 GGGAGTCCCTGGACACCTGCATGCTGCGACCCAGCGAGGCGCTGTTGTGACGCT 240
DB 181 GGGAGTCCCTGGACACCTGCATGCTGCGACCCAGCGAGGCGCTGTTGTGACGCT 240
OY 241 GGGGAGAGCCCTGTGGCGCCAGTGGGCTGTGTCTCTTGGATGAGGATACGGTACGCT 300
DB 241 GGGGAGAGCCCTGTGGCGCCAGTGGGCTGTGTCTCTTGGATGAGGATACGGTACGCT 300
OY 301 GAGGTGAATGGCCGACAGTACTGATGAGAGAGACTTTAAACCAATTGACAGGTCCTG 360
DB 301 GAGGTGAATGGCCGACAGTACTGATGAGAGAGACTTTAAACCAATTGACAGGTCCTG 360
OY 361 TGCCGCTGTGATGAGCGTGGCTTCACTGCTGCGCGCTGTGCAGTGAGGATGTGGGCTG 420
DB 361 TGCCGCTGTGATGAGCGTGGCTTCACTGCTGCGCGCTGTGCAGTGAGGATGTGGGCTG 420
OY 421 CCCAGCTGGAGCTGCCACGCCCCCAAGAGATAATACAGGTGACAGAAAGTCTGCCCGAG 480
DB 421 CCCAGCTGGAGCTGCCACGCCCCCAAGAGATAATACAGGTGACAGAAAGTCTGCCCGAG 480
OY 481 TGGGATGTGACAGGAGTGAACCGGATCCAGCGCTTCCAGCGGCGCAAGGACACCA 540
DB 481 TGGGATGTGACAGGAGTGAACCGGATCCAGCGCTTCCAGCGGCGCAAGGACACCA 540
OY 541 CTTTCTGCCCTTGTCACTGCTCTGCTGTGATGCTTGTTCANAATTGGACAGAGCC 600
DB 541 CTTTCTGCCCTTGTCACTGCTCTGCTGTGATGCTTGTTCANAATTGGAGACAGAGCC 600
OY 601 TGGGGCCCTGTCAACACACCTGTGGGCTGGGCGATAGCCACCCGAGTGTCCAACCAAG 660
DB 601 TGGGGCCCTGTCAACACACCTGTGGGCTGGGCGATAGCCACCCGAGTGTCCAACCAAG 660
OY 661 CGATTCTGCAACTGGAGATCCAAAGCGCGCTGTGTGTGCGCAGACCCCTGTGCGAGCC 720
DB 661 CGATTCTGCAACTGGAGATCCAAAGCGCGCTGTGTGTGCGCAGACCCCTGTGCGAGCC 720
OY 721 AGGAGCCACAGCTCATGGAACAGTCTTTCTAA 753
DB 721 AGGAGCCACAGCTCATGGAACAGTCTTTCTAA 753

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RESULT 2  
 us-10-010-408-1  
 ; Sequence 1, Application US/10010408  
 ; Publication No. US20020165185A1  
 ; GENERAL INFORMATION:

```

? APPLICANT: John J. Castellet, Jr.
? TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules
? and Uses Therefor
? NUMBER OF SEQUENCES: 13
? CORRESPONDENCE ADDRESS:
? ADDRESSER: LAHIVE & COCKFIELD, LLP
? CITY: Boston
? STREET: 28 State Street
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/010,408
? FILING DATE: 07-Dec-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/044,273
? FILING DATE: March 19, 1998
? APPLICATION NUMBER: <Unknown>
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Amy E. Mandragouras
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: MBT-004
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)742-4214
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1708 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 249..1001
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
? US-10-010-408-1
?
? Query Match 100.0%; Score 753; DB 15; Length 1708;
? Best Local Similarity 100.0%; Pred. No. 0;
? Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	361	TGCGCGCTGATGAGCGTGGCTTTCACCTCTCGCCGCTTGACGTAGAGATGTCGGCTG	420
Dp	609	TGCCCGCTGATGAGCGTGGCTTTCACCTCTCGCCGCTTGACGTAGAGATGTCGGCGTG	668
QY	421	CCCACTGGGACTGCCCAAGGCCCAAGAGAAATACAGTGGCCAGGAAGTGTGCCCCGAG	480
Dp	669	CCCACTGGGACTGCCCAAGGCCCAAGAGAAATACAGTGGCCAGGAAGTGTGCCCCGAG	728
QY	481	TGGGATATGTGACCAAGGAGATGACACCGCGGATCCAGCGCTCCACGGCGCACAGACACAA	540
Dp	729	TGGGATATGTGACCAAGGAGATGACACCGCGGATCCAGCGCGCTCCACGGCGCACAGACAA	788
QY	541	CTTTCTGGCCCTTGATACCTGCTCTGCTGTGATGCTCCCTGTGTCCAAAATTGGAGACACAGCC	600
Dp	789	CTTTCTGGCCCTTGATACCTGCTCTGCTGTGATGCTCCCTGTGTCCAAAATTGGAGACACAGCC	848
QY	601	TGGGGCCCTGTCTCAACCACTGTGGGCTGGGCAATAGCACCCGAGTGTCCAACCAAGAAC	660
Dp	849	TGGGGCCCTGTCTCAACCACTGTGGGCTGGGCAATAGCACCCGAGTGTCCAACCAAGAAC	908
QY	661	CGATTCTGCGCAACTGGAGATCCCAAGCGCCGCTGTCTGTGCCCCAGACCTGTGCGAGCC	720
Dp	909	CGATTCTGCGCAACTGGAGATCCCAAGCGCCGCTGTCTGTGCCCCAGACCTGTGCGAGCC	968
QY	721	AGGAGCCACAGCTCATGGAACAGTGGCTTTCTPA	753
Dp	969	AGGAGCCACAGCTCATGGAACAGTGGCTTTCTPA	1001

RESULT 3  
US-10-010-408-12

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:
:
: Sequence 12, Application US/10010408
: Publication No. US20020165185A1
:
: GENERAL INFORMATION:
:

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APPLICANT: John J. Castellote, Jr.  
TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced  
and Uses Therefor  
CCN-Like Molecules

;  
 ;  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ;  
 ;  
 ;

STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US

COUNTRY : USA  
ZIP : 02109  
COMPUTER READABLE FORM:  
\*\*\*\*\*  
MERRILL PARRISH

```

1      MEDIUM TYPE: floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      COMMANDER: Bobcat, Dinos, M10
5
6      Version: M1 3F

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1  SOFTWARE:  FalconWin Release #1.0, Version #1.25
2
3  CURRENT APPLICATION DATA:
4
5      APPLICATION NUMBER:  US/10/010,408
6
7      FILING DATE:  07-Dec-2001
8
9

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FILING DATE: 01-DEC-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004 273

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1 DOCKET NUMBER: 30, 207  
2  
3 REFERENCE/DOCKET NUMBER: MBI-004  
4  
5 TELECOMMUNICATION INFORMATION:  
6  
7 TELEPHONE: (617)227-7400

TELEPHONE: (617) 742-4214  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:

```

1  LENGTH: 681 base pairs
2
3  TYPE: nucleic acid
4
5  STRANDEDNESS: single
6

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;          TOPOLOGY: linear
;
; MOLECULE TYPE: CDNA

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;          FEATURE:
;          NAME/KEY : CDS
;          LOCATION : 1..681
;          SEQUENCE DESCRIPTION : SEQ ID NO: 12:
US-10-010-408-12

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Query Match	90.4%	Score 681;	DB 15;	Length 681;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 681;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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DB 1CAGC1G1GCGGACCC1G1ATCC1G1CC1G1GACACCA1CC1CA1G1CC1CA1GGGG1A 80

QY 130 CCGCTGGTGTGATGGCTGTGTGGCTGCTGAAAGTGTGTGCACGAGAGGTGGGGAGTCC 189

180 TGGGACCCATCTGCAATCTCTGCGGACCCCCAGCCAGGCGCTCGTTTCTGTCAGCTCTGGGGCAGGC 248  
Db 61 CCCCTGTGCTGATGGCTGTGCGCTGTCTAAAGTGTGTGCACCGAGGCGGGGGAGTCC 120

Db 121 TGGACACCACTGATGTCTGGCAGCCCCAGCAGGGCCTGGTTTGCAGCCCTGGGGCAGGC 180

**OY** 250 CCTGGGCGCCATGGGGCTGTGTCTCTTGGATGAGANTACGGTAGCTTGAGGTGAAT 309  
|||||  
**Dh** 181 CTGGGGCGCCATGGGGCTGTGTCTCTTGGATGAGANTACGGTAGCTTGAGGTGAAT 240  
|||||

310 GGCCGCAGGTACCTTGATGAGAGACCTTTAAACCCAAATTGCAGGGTCTGTGCCCTGT 369

Db 241 GGGCCGAGGTACCTGGATGGAGAGACCTTTAAACCCATTGCAAGGGTCCCTGTGCCCGCT 300

Ov 370 GATGACGGTGGCTTCACCTGCGCTCCGCTGTGACGTAGAGATGTGGCGCTGCCCAAGTCG 429

301 GATGACGGGTGGCTTCACCTGGCTCCGCTGTGTCAGTAGGATGTGGGGCTGCCACGCTGG 360

QY 430 GACTGCCACGCGCCCAAGAGATACAGTGCACAGAAAGTGCTGCCCGCAGTGGTATGT 489

Db 361 GACTGCCACGCGCCCAAGAGATACAGTGCACAGAAAGTGCTGCCCGCAGTGGTATGT 420

490 GACCAGGAGTGACACCGGCGATCCAGCGCTCCAGGCGCAGGACACCACTTTCTGCC 549

Db 421 GACCAGGGAGTGAACCCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTCTCGCC 480

Qy 550 CTTGTCACTCCTGCGCTCTGCTGATGTCCTCTTGTCCAAATTGGAGCACAGCCTTGAGGCCCC 609

Db 481 CTTCACACCTGCTGCTGATGCTCCCTGTCCAAATGGAGCAGCAGCTGGGGCCC 540

Qy 610 TGGCTAACCAACCTGTGGGCTGGGCGATAGCCACCCGAGTGTCCAAACAGAACCGATTCGC 669

Dbb 541 TGGCTAACCAACCTGTGGGCTGGGCGATAGCCACCCGAGTGTCCAAACAGAACCGATTCGC 600

670 CAACGTGAGATCCAAAGCCCGCTGTGTCTTGCCCAAGACCCCTGGCAGCCAGGAGCCAC 729

Db	60	CAACTGGACATCCAAACGGCCGCTGTGTCTGCCCCAGACCCCTGCCAGCCAGCAGGAGCCAC	bb
Qy	730	AGCTCATGAGACAGTGCCTTTC	750

Db 661 AGCTCATGACACAGTGCCTTC 681

RESULT 4  
US-10-010-408-8

```

; sequence 8 Application US/10010408
; Publication No. US20020165185A1
;
; GENERAL INFORMATION:
;
;   Port: 10408

```

APPLICANT: JOHN J. CASTELLINO, JR.  
 TITLE OF INVENTION: NO. US20020165185A1 Heparin-Induced CCN-Like Molecules and Uses Therefor  
 NUMBER OF SEQUENCES: 12

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
c/o: 28 State Street  
Camden, NJ 08102

SINCE: 20 State Street  
City: Boston  
STATE: Massachusetts

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <unknown>  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..210  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-010-408-8  
Query Match  
Best Local Similarity 27.9%; Score 210; DB 15; Length 210;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db  
1 CAGCTGTGCGGACACCCCTGACCTGTGCTGACACACCCAGTCCACAGGGGGTA 129  
|||  
130 CCGCTGTGCTGTGATGCGTGTGCTGTGTAAGTGTGTGACGAGAGCTGGGGAGTCC 189  
|||  
Db 61 CCGCTGTGCTGTGATGCGTGTGCTGTGTAAGTGTGTGACGAGAGCTGGGGAGTCC 120  
|||  
Qy 190 TGGCAGCACCTGTGATGTGTGACCCAGGAGGCTGTGTGTGACCTGGGGAGGC 249  
|||  
Db 121 TGGCAGCACCTGTGATGTGTGACCCAGGAGGCTGTGTGTGACCTGGGGAGGC 180  
|||  
Qy 250 CCGGCGGCATGGGGCTGTGTCTTGG 279  
|||  
Db 181 CCGGCGGCATGGGGCTGTGTCTTGG 210  
|||  
RESULT 5  
US-10-010-408-5  
Sequence 5, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castellot, Jr.  
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules  
and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESS: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <unknown>  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..177  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-010-408-5  
Query Match  
Best Local Similarity 23.5%; Score 177; DB 15; Length 177;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db  
1 TGTGAGTGATGAGCGCGGACCTGATGAGAGACCTTTAAACCAATTGAGGGTC 357  
|||  
Qy 358 CTGTCGCGCTGTGATGAGCGTGTGCTTCACTGCTGCTGCTGTGACGAGAGTGTGGG 417  
|||  
Db 61 CTGTCGCGCTGTGATGAGCGTGTGCTTCACTGCTGCTGCTGTGACGAGAGTGTGGG 120  
|||  
Qy 418 CTGCGACACTGGAGCTGCGCCAGGCGCCCAAGAGATACAGTGCAGGAAAGTGTGC 474  
|||  
Db 121 CTGCGACACTGGAGCTGCGCCAGGCGCCCAAGAGATACAGTGCAGGAAAGTGTGC 177  
|||  
RESULT 6  
US-10-010-408-10  
Sequence 10, Application US/10010408  
Publication No. US20020165185A1  
GENERAL INFORMATION:  
APPLICANT: John J. Castellot, Jr.  
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules  
and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESS: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/044,273  
FILING DATE: March 19, 1998  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MBI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-4214  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 174 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..174  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-010-408-10

Query Match 23.1%; Score 174; DB 15; Length 174;  
Best Local Similarity 100.0%; Pred. No. 3.3e-80;  
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 577 CCTGTCCAAATTTGAGACAGCCCTGGGGCCCTGCTACACCACTGTGGGCTGGGCATA 636  
Db 1 CCTGTCCAAATTTGAGACAGCCCTGGGGCCCTGCTACACCACTGTGGGCTGGGCATA 60  
Oy 637 GCCACCCGAGTGTCCACACGACGATTTGCCAACTGAGATCCACAGCCGCTGTGT 696  
Db 61 GCCACCCGAGTGTCCACACGACGATTTGCCAACTGAGATCCACAGCCGCTGTGT 120  
Oy 697 CTGCCACAGCCCTGCTGTGGCAGCCAGGACCAAGCTATGGAACAGTCTTTC 750  
Db 121 CTGCCACAGCCCTGCTGTGGCAGCCAGGACCAAGCTATGGAACAGTCTTTC 174

RESULT 7  
US-10-112-267-17  
Sequence 17, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: US/10/112,267  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156

SEQ ID NO 17  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-112-267-17

Query Match 12.0%; Score 90; DB 15; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.1e-36;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 162 AGTGTGTCACGAGAGGCTGGGGGAGTCTGTGACCACTGCATGTCTCGACCCAGCCA 221  
Db 418 AGTGTGTCACGAGAGGCTGGGGGAGTCTGTGACCACTGCATGTCTCGACCCAGCCA 477  
Oy 222 GGGCCTGTTGTGACGCTGGGGGAGGCC 251  
Db 478 GGGCCTGTTGTGACGCTGGGGGAGGCC 507

RESULT 8  
US-10-112-267-18/c  
Sequence 18, Application US/10112267  
Publication No. US20030068678A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David A.  
APPLICANT: Cohen, Robert  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Lawrence, David A.  
APPLICANT: Levine, Arnold J.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: P1176R2  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: US/10/112,267  
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/182,145B  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: US 60/063,704  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 18  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-112-267-18

Query Match 12.0%; Score 90; DB 15; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.1e-36;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 162 AGTGTGTCACGAGAGGCTGGGGGAGTCTGTGACCACTGCATGTCTCGACCCAGCCA 221  
Db 1317 AGTGTGTCACGAGAGGCTGGGGGAGTCTGTGACCACTGCATGTCTCGACCCAGCCA 1258  
Oy 222 GGGCCTGTTGTGACGCTGGGGGAGGCC 251  
Db 1257 GGGCCTGTTGTGACGCTGGGGGAGGCC 1228

RESULT 9  
US-09-864-761-23432  
Sequence 23432, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 23432  
LENGTH: 199  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL139352.8  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.00e-108  
OTHER INFORMATION: NT HIT: AF083500.1, EVALUATE 1.00e-108  
OTHER INFORMATION: SWISSPROT HIT: O19113, EVALUATE 9.00e-19  
US-09-864-761-23432  
Query Match 4.2%; Score 32; DB 10; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-864-761-6698  
Sequence 6698, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 6698  
LENGTH: 586  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL139352.8  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7  
US-09-864-761-6698  
Query Match 4.2%; Score 32; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 342 GAGGATGTGCGGCTGCCAGCTGGAGCTGCC 373

RESULT 11

US-10-112-267-38

Sequence 38, Application US/10112267

Publication No. US20030068678A1

GENERAL INFORMATION:

APPLICANT: Botstein, David A.

APPLICANT: Cohen, Robert

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Lawrence, David A.

APPLICANT: Levine, Arnold J.

APPLICANT: Pennica, Diane

APPLICANT: Roy, Margaret Ann

APPLICANT: Wood, William I.

TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: P117682

CURRENT APPLICATION NUMBER: US/10/112,267

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14

SEQ ID NO 38

LENGTH: 738

TYPE: DNA

ORGANISM: Homo sapiens

US-10-112-267-38

Query Match 4.2%; Score 32; DB 15; Length 738;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 GTACCCGTGCTGCTGGATGGCTGTGGCTGCTG 158

Db 115 GTACCCGTGCTGCTGGATGGCTGTGGCTGCTG 146

RESULT 12

US-10-112-267-39

Sequence 39, Application US/10112267

Publication No. US20030068678A1

GENERAL INFORMATION:

APPLICANT: Botstein, David A.

APPLICANT: Cohen, Robert

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Lawrence, David A.

APPLICANT: Levine, Arnold J.

APPLICANT: Pennica, Diane

APPLICANT: Roy, Margaret Ann

APPLICANT: Wood, William I.

TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: P117682

CURRENT APPLICATION NUMBER: US/10/112,267

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 156

SEQ ID NO 39

LENGTH: 841

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: misc-feature

LOCATION: 1-841

OTHER INFORMATION: Sequence is synthesized.

US-10-112-267-39

Query Match 4.2%; Score 32; DB 15; Length 841;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 406 GAGGATGTGCGGCTGCCAGCTGGAGCTGCC 437

Db 417 GAGGATGTGCGGCTGCCAGCTGGAGCTGCC 448

RESULT 13

US-10-137-866-319

Sequence 319, Application US/10137866

Publication No. US20030129689A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Geo, Wei-Qiang

APPLICANT: Gerltsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C151

CURRENT APPLICATION NUMBER: US/10/137,866

PRIOR FILING DATE: 2002-05-03

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059836

PRIOR FILING DATE: 1997-09-24

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062285

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062287	PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814	PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816	PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045	PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082	PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063127	PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327	PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329	PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550	PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561	PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704	PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733	PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735	PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738	PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755	PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248	PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809	PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186	PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846	PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066511	PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453	PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770	PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212	PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278	PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334	PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694	PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320	PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612	PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086	PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 60/074092	PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 60/077791	PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079653	PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728	PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165	PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/081203
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081229
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081655
PRIOR FILING DATE:	1998-04-14
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081818
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082999
PRIOR FILING DATE:	1998-04-24
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083545
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084627
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084637
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085149
PRIOR FILING DATE:	1998-05-12
PRIOR APPLICATION NUMBER:	60/085323
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085338
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085399
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085579
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085697
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085704
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/086414
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/086430
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/087106
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/088026
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/0880730
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088741
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088810
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088858
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/089322
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089599
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090538
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090863
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091360
PRIOR FILING DATE:	1998-07-01

PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091982

Query Match 4.2%; Score 32; DB 14; Length 1266;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTGTGATGGCTGTGCTGCTG 158  
DB 136 GTACCCCTGGTGTGATGGCTGTGCTGCTG 167

RESULT 14  
US-10-146-726-319  
Sequence 319, Application US/10146726  
Publication No. US20030129690A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C308  
CURRENT APPLICATION NUMBER: US/10/146,726  
CURRENT FILING DATE: 2002-05-15  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 319  
LENGTH: 1266  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-146-726-319

Query Match 4.2%; Score 32; DB 14; Length 1266;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTGTGATGGCTGTGCTGCTG 158  
DB 136 GTACCCCTGGTGTGATGGCTGTGCTGCTG 167

RESULT 15  
US-10-146-727-319  
Sequence 319, Application US/10146727  
Publication No. US20030129691A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C312  
CURRENT APPLICATION NUMBER: US/10/146,727  
CURRENT FILING DATE: 2002-05-15  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 319  
LENGTH: 1266  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-146-727-319

Query Match 4.2%; Score 32; DB 14; Length 1266;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTGTGATGGCTGTGCTGCTG 158  
DB 136 GTACCCCTGGTGTGATGGCTGTGCTGCTG 167

Search completed: July 28, 2003, 15:36:37  
Job time: 185.44 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:16:26 ; Search time 1335.79 Seconds  
(without alignments)  
9129.604 Million cell updates/sec

Title: US-10-010-408-3  
Perfect score: 753  
Sequence: 1 ATGAGGGGAGCCCACTGAT.....CATGACAGTGTCTTCTAA 753

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	12.0	940	14	B0937887
2	67	8.9	537	14	B0560868
3	49	6.5	424	10	BB849097
4	35	4.6	488	9	AA754979
5	35	4.6	966	12	BF141695
6	32	4.2	380	12	BG900020

7	32	4.2	405	12	BG900069
8	32	4.2	489	14	BM751866
9	32	4.2	618	12	BG538695
10	32	4.2	620	13	BG928868
11	32	4.2	651	13	BI457141
12	32	4.2	749	9	AL555144
13	32	4.2	750	13	BM043988
14	32	4.2	790	13	BM046275
15	32	4.2	800	13	BI826781
16	32	4.2	886	13	BI822142
17	32	4.2	888	13	BI825652
18	32	4.2	916	13	BI457367
19	32	4.2	928	13	BI161474
20	32	4.2	933	14	B0278961
21	32	4.2	979	14	B0279131
22	32	4.2	1006	14	BM921531
23	32	4.2	1022	14	B0952960
24	32	4.2	1058	14	BM805088
25	32	4.2	1073	14	B0073722
26	32	4.2	1166	13	BM543799
27	32	4.2	1251	14	B0961357
28	28	3.7	762	14	B0195526
29	24	3.2	426	9	AA717584
30	23	3.1	436	17	A0095651
31	23	3.1	742	13	BI758148
32	23	3.1	792	13	BI823598
33	21	2.8	495	13	BI204749
34	21	2.8	529	9	AI897896
35	21	2.8	561	12	BF051668
36	21	2.8	563	9	AI897344
37	21	2.8	609	37	AI485142
38	21	2.8	620	10	AW223381
39	20	2.7	188	14	H55466
40	20	2.7	319	13	BM389674
41	20	2.7	334	14	BM698298
42	20	2.7	372	12	BE918366
43	20	2.7	381	20	BE537338
44	20	2.7	391	14	W80867
45	20	2.7	401	12	BF849398

#### ALIGNMENTS

RESULT 1  
LOCUS B0937887 940 bp mRNA linear EST 21-AUG-2002  
DEFINITION AGENCOURT\_8951807 NCI\_CGAP\_Co24 Mus musculus CDNA clone  
IMAGE:6476852 5', mRNA sequence.  
ACCESSION B0937887  
VERSION B0937887.1 GI:22353365  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 940)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNL at:  
<http://image.llnl.gov>  
Plate: LLM14017 row: n column: 21  
High quality sequence stop: 543.  
Location/Qualifiers  
1..940

FEATURES  
source



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/tissue_type="inner ear"
/dev_stage="adult"
/note="pooled tissues : (tissue_type=cerebellum,
dev stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=males), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"
BASE COUNT      65 a      124 c      132 g      103 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-13;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTCACGAGCGAGGAGTCTCTGCGACCATCGATGCTGTC 210
DB 373 AGTGTGTCACGAGCGAGGAGTCTCTGCGACCATCGATGCTGTC 421

RESULT 4
LOCUS AA754979 488 bp mRNA linear EST 21-JAN-1998
DEFINITION vu55g08.r1 Soares mammary_gland_NBMG Mus musculus cDNA clone
IMAGE:1195358 5', mRNA sequence.
ACCESSION AA754979
VERSION AA754979.1 GI:2802177
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 488)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:642454
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 478.
Location/Qualifiers
1..488
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1195358"
/clone_lib="Soares_mammary_gland_NBMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTCACATCTGAGTGGAGCGCGCCGCGATGCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73D vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library

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constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT      110 a      138 c      130 g      110 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 TCCACGACGACCGGATTTGCGCACTGGAGATCCA 683
DB 14 TCCACGACGACCGGATTTGCGCACTGGAGATCCA 48

RESULT 5
LOCUS BF141695 966 bp mRNA linear EST 24-OCT-2000
DEFINITION 601790752P1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021308 5',
mRNA sequence.
ACCESSION BF141695
VERSION BF141695.1 GI:10980735
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 966)
NIH-MGC http://mgc.nci.nih.gov/.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM9276 row: h column: 13
High quality sequence stop: 613.
Location/Qualifiers
1..966
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:4021308"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model MMTV-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      227 a      298 c      258 g      183 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 TCCACGACGACCGGATTTGCGCACTGGAGATCCA 683
DB 90 TCCACGACGACCGGATTTGCGCACTGGAGATCCA 124

RESULT 6
LOCUS BG900020 380 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA48-I-G2.R HOA (Human Osteoarthritis Cartilage) Homo sapiens cDNA
, mRNA sequence.
ACCESSION BG900020

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VERSION      BG900020.1  GI:14310269
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
              1 (bases 1 to 380)
              Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
              Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
              Lark,M.W.
              Identification and initial characterization of 5000 expressed
              sequenced tags (ESTs) each from adult human normal and
              osteoarthritic cartilage cDNA libraries
              Osteoarthr. Cartil. 9 (7), 641-653 (2001)
              21482651
COMMENT      Contact: Sanjay Kumar
              UM2109
              GlaxoSmithKline
              709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
              Tel: 610-270-7245
              Fax: 610-270-5598
              Email: sanjay_kumar-1@gsk.com
              Seq primer: 17.

FEATURES
  source
    1..380
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="HOA (Human Osteoarthritic Cartilage)"
    /tissue_type="cartilage"
    /lab_host="E.coli DH10 B"
    /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
    Directional"

BASE COUNT   58 a 139 c 118 g 65 t

ORIGIN
Query Match      4.2%; Score 32; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGCTGCTGCTGCTG 158
    |||||||||||||||||||||||||||||||
Db 206 GTACCCCTGCTGCTGATGCTGCTGCTGCTG 237

RESULT 7
LOCUS       BG900069          405 bp      mRNA      linear      EST 06-NOV-2001
DEFINITION  HOA51-1-A11.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
ACCESSION  BG900069
VERSION    BG900069.1  GI:14310318
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
            1 (bases 1 to 405)
            Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
            Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
            Osteoarthr. Cartil. 9 (7), 641-653 (2001)
            21482651
COMMENT    Contact: Sanjay Kumar
            UM2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: 17.

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```

FEATURES
  source
    Location/Qualifiers
    1..405
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="HOA (Human Osteoarthritic Cartilage)"
    /tissue_type="cartilage"
    /lab_host="E.coli DH10 B"
    /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
    Directional"

BASE COUNT   62 a 140 c 135 g 68 t

ORIGIN
Query Match      4.2%; Score 32; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGCTGCTGCTGCTG 158
    |||||||||||||||||||||||||||||||
Db 202 GTACCCCTGCTGCTGATGCTGCTGCTGCTG 233

RESULT 8
LOCUS       BM751866          489 bp      mRNA      linear      EST 04-MAR-2002
DEFINITION  K-EST0028180 S2SNU668s1 Homo sapiens cDNA clone S2SNU668s1-2-D09
ACCESSION  BM751866
VERSION    BM751866.1  GI:19081484
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
            1 (bases 1 to 489)
            Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Kim,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
            21C Frontier Korean EST Project 2001
            Unpublished (2002)
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@email.kribb.re.kr
            Plate: 2 row: D column: 09
            High quality sequence stop: 489.
            Location/Qualifiers
            1..489
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="S2SNU668s1-2-D09"
            /clone_lib="S2SNU668s1"
            /sex="M"
            /tissue_type="Ascites"
            /cell_type="Epithelial"
            /cell_line="SNU-668"
            /lab_host="Top10F"
            /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
            Site_2: NotI; The poly (A)+ RNA was deapped with tobacco
            acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
            including EcoRI site by treatment of T4 RNA ligase. The
            first strand cDNA was synthesized from oligo dt-selected
            mRNA by priming with dr-tailed vector. The dr-tailed
            vector was adjusted to have about 60nt. The cDNA vector
            was circularized with E. coli DNA ligase after digestion
            of EcoRI which site is also included in vector. An RNA
            strand converted to a DNA strand by Okayama-Berg method.
            The obtained cDNA vectors were used for transposition method.
            After analyzing and sequencing about 2,000 - 3,000
            colonies in original cDNA library, the abundant cDNAs were

```

selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli TOP10<sup>®</sup> with electroporation method."

coll TOP10<sup>®</sup> with electroporation method."

BASE COUNT 75 a 173 c 159 g 82 t

ORIGIN

Query Match 4.2%; Score 32; DB 14; Length 489;  
Best Local Similarity 100.0%; Pred. No. 8.2e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 406 GAGGATGTCGCGCTGCCAGCTGGAGTCCCC 437  
|||||  
DB 139 GAGGATGTCGCGCTGCCAGCTGGAGTCCCC 170

RESULT 9 618 bp mRNA linear EST 03-APR-2001  
LOCUS BG538695  
DEFINITION 602566932P1 NIH\_MGC\_77 Homo sapiens CDNA clone IMAGE:4691574 5',  
mRNA sequence.  
ACCESSION BG538695  
VERSION BG538695.1 GI:13530928  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 618)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNLS Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LINC1510 row: P column: 07  
High quality sequence stop: 499.

#### FEATURES

##### SOURCE

1. 618  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4691574"  
/clone\_lib="NIH\_MGC\_77"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcgccctcgcc); Site\_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTGAGAGCGCGAGCGCGAGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

BASE COUNT 95 a 194 c 213 g 116 t

ORIGIN

Query Match 4.2%; Score 32; DB 12; Length 618;  
Best Local Similarity 100.0%; Pred. No. 8.5e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 GTACCCCTGCTGCTGATGCTGCTGCTG 158  
|||||  
DB 291 GTACCCCTGCTGCTGATGCTGCTGCTG 322

RESULT 10 620 bp mRNA linear EST 06-NOV-2001  
LOCUS BG928868  
DEFINITION HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA  
Sequence.  
ACCESSION BG928868  
VERSION BG928868.1 GI:14323391  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 620)  
AUTHORS Kumar,S., Connor,J.R., Dadds,R.A., Halsey,M., Van Horn,M., Mao,J., Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.  
TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
JOURNLS Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
COMMENT Contact: Sanjay Kumar  
Email: sanjay\_kumar-1@gsf.com  
Seq primer: 17.

FEATURES  
source  
Location/Qualifiers  
1. 620  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

BASE COUNT 97 a 218 c 207 g 98 t

ORIGIN

Query Match 4.2%; Score 32; DB 13; Length 620;  
Best Local Similarity 100.0%; Pred. No. 8.5e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 GTACCCCTGCTGCTGATGCTGCTGCTG 158  
|||||  
DB 210 GTACCCCTGCTGCTGATGCTGCTGCTG 241

RESULT 11 651 bp mRNA linear EST 21-AUG-2001  
LOCUS B1457141  
DEFINITION 603185392P1 NIH\_MGC\_42 Homo sapiens CDNA clone IMAGE:5258159 5',  
mRNA sequence.  
ACCESSION B1457141  
VERSION B1457141.1 GI:15247797  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 651)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNLS Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM1869 row: 9 column: 24  
 High quality sequence stop: 651.

# FEATURES

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1. 651

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5258159"

/clone\_1lb="NIH\_MGC\_42"

/tissue\_type="epithelioid carcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT

91 a 230 c 219 g 111 t

Query Match

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS

BM043988

DEFINITION

603620978P1 NIH\_MGC\_40 Homo sapiens CDNA clone IMAGE:5446794 5',

ACCESSION

BM043988

VERSION

BM043988.1 GI:16773255

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 750)

NIH-MGC <http://mgs.ccl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: DCTD/DP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM1929 row: k column: 19

High quality sequence stop: 714.

Location/Qualifiers

1. 750

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5446794"

/clone\_1lb="NIH\_MGC\_40"

/tissue\_type="carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: prostate; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT

112 a 267 c 246 g 125 t

Query Match

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS

BM046275

DEFINITION

790 bp mRNA linear EST 07-NOV-2001

ACCESSION

BM046275

VERSION

BM046275.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 749)

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 749)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

Location/Qualifiers

1. 749

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CSODK007021"

/clone\_1lb="L1L\_NFL006\_P12"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive

BASE COUNT

127 a 267 c 246 g 125 t

Query Match

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS

BM046275

DEFINITION

790 bp mRNA linear EST 07-NOV-2001

ACCESSION

BM046275

VERSION

BM046275.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 749)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

Location/Qualifiers

1. 749

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CSODK007021"

/clone\_1lb="L1L\_NFL006\_P12"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive

BASE COUNT

127 a 267 c 246 g 125 t

Query Match

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS

BM046275

DEFINITION

790 bp mRNA linear EST 07-NOV-2001

ACCESSION

BM046275

VERSION

BM046275.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 749)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

Location/Qualifiers

1. 749

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CSODK007021"

/clone\_1lb="L1L\_NFL006\_P12"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive

BASE COUNT

127 a 267 c 246 g 125 t

Query Match

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS

BM046275

DEFINITION

790 bp mRNA linear EST 07-NOV-2001

ACCESSION

BM046275

VERSION

BM046275.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 749)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

Location/Qualifiers

1. 749

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CSODK007021"

/clone\_1lb="L1L\_NFL006\_P12"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive

BASE COUNT

127 a 267 c 246 g 125 t

Query Match

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS

BM046275

DEFINITION

790 bp mRNA linear EST 07-NOV-2001

ACCESSION

BM046275

VERSION

BM046275.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 749)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

DEFINITION 603626068F1 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:5452480 5', mRNA sequence.  
 ACCESSION BM046275  
 VERSION BM046275.1 GI:16775542  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 790)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCM/DMP  
 cDNA Library Preparation: Ling Hong/Rudin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LICM1944 row: h column: 17  
 High quality sequence stop: 780.  
 Location/Qualifiers  
 1..790  
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 /clone="IMAGE:5452480"  
 /clone\_1id="NIH\_MGC\_40"  
 /tissue\_type="carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: prostate; Vector: pOTB7; site\_1: XhoI; site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
 BASE COUNT 121 a 265 c 269 g 135 t  
 ORIGIN  
 Query Match 4.2%; Score 32; DB 13; Length 790;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 406 GAGGATGTGGCGTCCGAGCTGGAGCTGCC 437  
 ||||||||||||||||||||||||||||||||  
 Db 265 GAGGATGTGGCGTCCGAGCTGGAGCTGCC 296  
 RESULT 15  
 B1826781 800 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603077268F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5169065 5', mRNA sequence.  
 DEFINITION B1826781  
 ACCESSION B1826781  
 VERSION B1826781.1 GI:15938331  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 800)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: L1AM11420 row: g column: 18  
 High quality sequence stop: 788.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5169065"  
 /clone\_1id="NIH\_MGC\_119"  
 /tissue\_type="medulla"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-SPORT6; site\_1: NotI; site\_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."  
 BASE COUNT 115 a 284 c 264 g 136 t 1 others  
 ORIGIN  
 Query Match 4.2%; Score 32; DB 13; Length 800;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 127 GTACCCCTGTCGTGATGCTGTGGCTGCTG 158  
 ||||||||||||||||||||||||||||||||  
 Db 120 GTACCCCTGTCGTGATGCTGTGGCTGCTG 151

Search completed: July 28, 2003, 18:02:13  
 Job time : 1335.79 secs

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